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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE  
EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene  
expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the  
brain and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

20

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto\_BRAIN.txt, created 25 24 January 2001, having 25,840,972 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome- 35 derived single exon nucleic acid probes expressed in human



brain and single exon nucleic acid microarrays that include such probes.

### Background of the Invention

5           For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

          For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

          More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

          One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,  
Science 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches – and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species – there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of  
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,  
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the  
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many  
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that  
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting  
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et  
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,  
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.  
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic  
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*  
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily  
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach  
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries  
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex  
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

          Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that  
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.  
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

### 30 Summary of the Invention

          The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional  
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel  
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids  
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single  
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably  
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality  
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000  
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a  
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,  
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least  
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is  
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane  
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,  
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:



12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring  
5 human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high  
10 stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the  
15 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon  
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,  
25 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent  
35 labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

20 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

30 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

35 wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon  
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,  
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in  
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types  
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ  
35 ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for  
10 electronic search, query, and analysis of such annotated sequence.

### Detailed Description of the Invention

15

#### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each  
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called  
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books  
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary  
35 planar substrate, as is described, *inter alia*, in Brenner

et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5           As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick  
10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

          As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid  
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the  
20 requirement that the probe hybridize to mRNA.

          As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence  
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

          As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing  
30 the predicted exon.

          As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a  
35 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a  
5 portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a  
10 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF  
15 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another  
20 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit  
25 specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual  
35 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

### Brief Description of the Drawings

The present invention is further illustrated with  
10 reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and  
15 associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional  
20 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of  
25 ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described,  
30 of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed  
35 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original



sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence  
5 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A  
10 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

15 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can  
20 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part  
25 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100  
30 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the  
35 National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic  
5 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by  
10 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of  
15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into  
20 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will  
25 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental  
30 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the  
35 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often  
5 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the  
10 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within  
15 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

20 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

25 FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and  
30 facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or  
35 interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the  
5 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously  
10 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily  
15 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other  
20 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity  
25 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10)  
30 ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query  
35 criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable  
5 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,  
10 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and  
15 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual  
20 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,  
25 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known  
30 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be  
35 removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired  
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower  
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest  
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,  
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as  
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting  
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating  
35 transcription, regulating message transport after



transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability  
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function  
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as  
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for  
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)  
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene  
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;  
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison  
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the  
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process  
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to  
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon  
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene  
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible  
35 secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the  
5 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with  
10 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

15 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer  
20 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify  
25 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

30 Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it  
35 has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5           The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic  
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased  
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves  
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later  
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least  
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for  
35 amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, 5 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 10 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

15 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 20 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 25 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

30 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 35 readily be used. As further described in Example 1, 16 or



32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create  
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.  
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using  
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on  
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.  
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads  
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high  
35 throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will  
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one  
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created  
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or  
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al.,  
or from the *de novo* construction of "problem specific"  
30 libraries targeted at a particular biological question, R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST, microarrays".

Such EST microarrays by definition can measure  
35 expression only of those genes found in EST libraries,

shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective  
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be  
10 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the  
15 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA  
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present  
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse  
35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,  
5 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric  
10 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-  
15 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present  
20 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the  
25 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically  
30 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector  
35 sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly  
5 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through  
10 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-  
15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker  
20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include  
25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to  
30 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without  
35 such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such  
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present  
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual  
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be  
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often  
25 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized  
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large



percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower  
5 percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual  
10 probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the  
15 present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear  
20 genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the  
25 ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present  
30 invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence  
35 drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which  
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization  
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the  
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can  
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see  
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of  
35 nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As  
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are  
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain  
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for  
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived  
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate  
35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits  
5 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-  
10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'  
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

20 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

25 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered  
30 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing  
35 information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate  
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a  
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental  
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be  
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide  
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local  
35 alignment search tool"). The results of such query -

including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence -- can then be passed directly to process 500, or used to  
5 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data  
10 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or  
15 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or  
20 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence  
25 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic  
30 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given  
35 the number of nucleotides typically represented in an

annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left  
5 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10               As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides  
15 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other  
20 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.  
25 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or  
30 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity  
35 or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection  
5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional  
10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

15 Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method  
20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c  
30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.  
35 For example, rectangles 83a can represent the results from



GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links  
5 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be  
10 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical  
15 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of  
20 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of  
25 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to  
30 depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to  
35 indicate expression intensity. As discussed *infra*, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

#### Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of  
5 the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon  
15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these  
20 ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in  
25 brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness  
30 of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades  
35 Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5           Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence  
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2  
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

          Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic  
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and  
25 internal neurofibrillary tangles.

          Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., Acta Psychiat. Neurol. Scand. 82(suppl.): 1-152 (1952).

30           At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding  
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be



temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing  
5 (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological  
15 transmission, leading to diminished or lost function. Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual impairment, due to inflammation of the optic nerve, termed  
20 optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple  
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general population, but could discern no definite genetic pattern  
30 of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet.  
7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to  
35 the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset  
5 is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others  
10 improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent  
15 simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of  
20 controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25  
25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of  
30 schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21,  
35 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2  
different sites, as have sites on the X chromosome. Wei et  
al., Nature Genet. 25:376-377 (2000) report more  
specifically that the NOTCH4 locus is associated with  
5 susceptibility to schizophrenia.

In general, however, it is believed that  
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.  
8:1729-1739 (1999) undertook a systematic search for  
10 linkage in 196 affected sib pairs (ASPs) with  
schizophrenia. Using 229 microsatellite markers at an  
average intermarker distance of 17.26 cM, followed in a  
second stage by a further 54 markers allowing the regions  
identified in stage 1 to be typed at an average spacing of  
15 5.15 cM, Williams et al. considered results on chromosomes  
4p, 18q, and Xcen as suggestive; however, given the scores,  
Williams et al. interpreted their results as suggesting  
that common genes of major effect (susceptibility ratio  
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.  
81(5):364-76 (1998), in a genome-wide search for  
schizophrenia susceptibility genes, found that twelve  
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and  
22) had at least one region with a nominal P value <0.05,  
25 that two of these chromosomes had a nominal P value <0.01  
(chromosomes 13 and 16), and that five chromosomes (1, 2,  
4, 11, and 13) had at least one marker with a lod score  
>2.0, suggesting the existence of multiple loci that  
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are  
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,  
paroxysmal disorders of cerebral function (seizures); that  
is, by sudden, brief attacks of altered consciousness,  
35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically  
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion diseases (Creutzfeld-Jakob, Gerstmann-Straussler-Shenker,  
10 familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-telangiectasia, amyotrophic lateral sclerosis, bulbo-spinal  
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease,  
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man syndrome and Von Hippel-Lindau  
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma,  
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous  
35 system that likely have genetic components include the

various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10           The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20           For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

          In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be  
5 used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's  
10 genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at  
15 sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the  
20 probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence  
25 of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which  
30 the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of  
35 only 11%, whereas 36% of ORFs whose expression was



measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5           Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10           The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15           Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20           Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);

35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine  
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,  
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and  
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the  
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,  
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway  
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter  
5 a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile  
10 and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

15 Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-  
20 derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

25 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules  
30 so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,  
35 morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047;  
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a  
form and quantity suitable for amplification, where the  
5 amplified product is thereafter to be used in the  
hybridization reactions that probe gene expression.  
Typically, such probes are provided in a form and quantity  
suitable for amplification by PCR or by other well known  
amplification technique. One such technique additional to  
10 PCR is rolling circle amplification, as is described, *inter*  
*alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and  
international patent publications WO 97/19193 and  
WO 00/15779. As is well understood, where the probes are  
to be provided in a form suitable for amplification, the  
15 range of nucleic acid analogues and/or internucleotide  
linkages will be constrained by the requirements and nature  
of the amplification enzyme.

Where the probe is to be provided in form  
suitable for amplification, the quantity need not be  
20 sufficient for direct hybridization for gene expression  
analysis, and need be sufficient only to function as an  
amplification template, typically at least about 1, 10 or  
100 pg or more.

Each discrete amplifiable probe can also be  
25 packaged with amplification primers, either in a single  
composition that comprises probe template and primers, or  
in a kit that comprises such primers separately packaged  
therefrom. As earlier mentioned, the ORF-specific  
5' primers used for genomic amplification can have a first  
30 common sequence added thereto, and the ORF-specific 3'  
primers used for genomic amplification can have a second,  
different, common sequence added thereto, thus permitting,  
in this embodiment, the use of a single set of 5' and 3'  
primers to amplify any one of the probes. The probe  
35 composition and/or kit can also include buffers, enzyme,

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 – 25,434, respectively, for probe SEQ ID NOS. 1 – 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

5           Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a  
10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization  
15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room  
20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single  
25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more  
30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more  
35 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be  
5 provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural  
10 individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

15 If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of  
20 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

25 In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention,  
30 as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other  
35 conventional means, as are described, *inter alia*, in



Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term  
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.  
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the  
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray  
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a  
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means  
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon  
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 - 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of  
5 illustration and not by way of limitation.

#### EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted  
in Human Genomic Sequence

10

#### Bioinformatics Results

All human BAC sequences in fewer than 10 pieces  
that had been accessioned in a five month period  
immediately preceding this study were downloaded from  
15 GenBank. This corresponds to ~2200 clones, totaling ~350  
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the  
program CROSS\_MATCH, the sequence was analyzed for open  
reading frames using three separate gene finding programs.  
20 The three programs predict genes using independent  
algorithmic methods developed on independent training sets:  
GRAIL uses a neural network, GENEFINDER uses a hidden  
Markoff model, and DICTION, a program proprietary to  
Genetics Institute, operates according to a different  
25 heuristic. The results of all three programs were used to  
create a prediction matrix across the segment of genomic  
DNA.

The three gene finding programs yielded a range  
of results. GRAIL identified the greatest percentage of  
30 genomic sequence as putative coding region, 2% of the data  
analyzed. GENEFINDER was second, calling 1%, and DICTION  
yielded the least putative coding region, with 0.8% of  
genomic sequence called as coding region.

The consensus data were as follows. GRAIL and  
35 GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding  
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a  
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

#### 15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes  
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,  
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3  
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit  
35 subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant  
5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR<sup>®</sup> green (Molecular Probes, Inc., Eugene, OR) staining of  
15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest  
20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range  
25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region,  
30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process  
35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

5                    Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and  
10 standard protocols.

                  Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some  
15 submitted sequence data.

                  Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression  
20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not  
25 shown).

                  The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII  
30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

35                    Each of the probe sequences was BLASTed against

the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

## EXAMPLE 2

### Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,



100 $\mu$ M dATP, 100  $\mu$ M dGTP, 100  $\mu$ M dTTP, 50  $\mu$ M dCTP, 50  $\mu$ M  
Cy3-dCTP or Cy5-dCTP 50  $\mu$ M, and 200 U Superscript II  
enzyme. The reaction was incubated for 2 hours at 42°C.  
After 2 hours, the first strand cDNA was isolated by adding  
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.  
The reaction was then purified using a Qiagen PCR cleanup  
column, increasing the number of ethanol washes to 5.  
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured  
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA  
corresponding to 50 pmoles of each dye were then dried in a  
Speedvac, resuspended in 30  $\mu$ l hybridization solution  
containing 50% formamide, 5X SSC, 0.2  $\mu$ g/ $\mu$ l poly(dA), 0.2  
 $\mu$ g/ $\mu$ l human c<sub>0</sub>t1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a  
coverslip, with the array placed in a humid oven at 42°C  
overnight. Before scanning, slides were washed in 1X SSC,  
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%  
SDS, at 55°C for 20 minutes. Slides were briefly dipped in  
20 water and dried thoroughly under a gentle stream of  
nitrogen.

Slides were scanned using a Molecular Dynamics  
Gen3 scanner, as described. Schena (ed.), Microarray  
Biochip: Tools and Technology, Eaton Publishing  
25 Company/BioTechniques Books Division (2000) (ISBN:  
1881299376).

Although the use of pooled cDNA as a reference  
permitted the survey of a large number of tissues, it  
attenuates the measurement of relative gene expression,  
30 since every highly expressed gene in the tissue/cell type-  
specific fluorescence channel will be present to a level of  
at least 10% in the control channel. Because of this fact,  
both signal and expression ratios (the latter hereinafter,  
"expression" or "relative expression") for each probe were  
35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Expressed Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca<sup>2+</sup> binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
 10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
 15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed  
 20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless  
 25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to



tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2  
were similar to actin (AL035701-2; AL034402-1), and 6 were  
found to be homologous to glyceraldehyde-3-phosphate  
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,  
5 AC006064-K; AC035604-3; AC006064-L). These genes are often  
used as controls or housekeeping genes in microarray  
experiments of all types.

Other interesting genes highly expressed in brain  
were a ferritin heavy chain protein, which is reported in  
10 the literature to be found in brain and liver (Joshi et  
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result  
duplicated with the array. Other highly expressed chip  
sequences included a translation elongation factor 1 $\alpha$   
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-  
15 chromosome RNA-binding motif (Chai et al., *Genomics*  
49(2):283-89 (1998)) (AC007320-3). A low homology analog  
(AP00123-1/2) to a gene, DSCR1, thought to be involved in  
trisomy 21 (Down's syndrome), showed high expression in  
both brain and heart, in agreement with the literature  
20 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we  
selected the BAC AC006064 to be included on the array.  
This BAC was known to contain the GAPDH gene, and thus  
could be used as a control for the ORF selection process.  
25 The gene finding and exon selection algorithms resulted in  
choosing 25 exons from BAC AC006064 for spotting onto the  
array, of which four were drawn from the GAPDH gene. Table  
3 shows the comparison of the average expression ratio for  
the 4 exons from BAC006064 compared with the average  
30 expression ratio for 5 different dilutions of a  
commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control ( n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$
Lung	-4.95 $\pm$ 0.93	-3.75 $\pm$ 0.21
Placenta	-3.56 $\pm$ 0.25	-3.52 $\pm$ 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

20

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they  
5 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):  
red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
10 turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

#### 15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,  
20 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe  
25 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-  
30 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented  
35 fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOs.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

5 The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.  
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because  
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the  
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were  
35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;



(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

#### EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid  
5 probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid  
10 probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of  
25 single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human  
gene expression in a sample derived from human brain  
30 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of  
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

16. A single exon nucleic acid probe as claimed in any one.  
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one  
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one  
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

5       contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then  
10       measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15       algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are derived from mRNA from the brain of said eukaryote, said probe is a  
20       single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

30       identifying a plurality of exons from genomic sequence according to the method of claim 23; and then  
measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,  
35       wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID  
5 NOS: 1 - 25,434 which encodes a peptide.
26. A peptide encoded by a sequence as set out in any of  
SEQ ID Nos: 1 - 25,434.
- 10 27. A peptide comprising a sequence as set out in any of  
SEQ ID NOS: 25,435 - 37,811.

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	25968	6.47				
869	13638	26308	15.92				
1022	13782		2.16				
1279	14029	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1609	14353	27044	3.19				
1633	14379	27068	6.1				
1718	14461	27160	3.31				
1743	14485	27184	1.44				
1750	14492	27192	6.78				
1884	14621	27331	1.44				
1971	14707	27425	2.14				
2162	14882	27627	2.7				
2277	15003	27743	2.91				
2578	15292	28028	1				
2578	15292	28029	1				
3181	16844	28595	2.83				
3442	16198	28848	1.42				
3505	16261	28915	12.04				
3549	16304		1				
3649	16402	29042	1.67				
3928	16678		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29613	0.97				
4248	16989	29614	0.97				
4303	17042		1.07				
4361	17089	29734	0.76				
4784	17516	30138	0.99				
4983	17706	30310	6.38				
4985	17718	30323	1.3				
5176	17985	30500	1.57				
5176	17985	30501	1.57				

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5336	18139		4.3				
5510	18308		6.14				
5593	18139		3.97				
5648	18443	31358	0.6				
5654	18449	31362	3.28				
5832	25082	31673	1.62				
5958	18740	31699	1.75				
6322	19092		1.27				
6454	19222	32220	1.1				
6454	19222	32221	1.1				
7025	19717	32774	1				
7025	19717	32775	1				
7311	19894	33071	1.76				
7311	19894	33072	1.76				
7712	20376		0.61				
7960	20655	33780	1.4				
8384	21077	34214	1.49				
8759	21451	34598	0.59				
8759	21451	34599	0.59				
9434	22112	35287	2.67				
9606	22318	35515	0.77				
9782	22433	35638	1.24				
9922	22570	35767	0.94				
10328	22875	36194	0.62				
10328	22875	36195	0.62				
10682	23277		2.83				
10749	25131	36679	1.34				
10852	23628		2.2				
11030	23701	36868	1.84				
11332	24023	37328	2.02				
11485	24086		2.47				
12313	24735		1.52				
12609	24916	31006	2.36				
5961	18743	31703	17.79	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18



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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7905	20600	33730	1.74	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9843	22295	35489	0.44	9.8E+00	Y18830.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9843	22295	35489	0.44	9.8E+00	Y18830.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
8901	19639	32884	0.73	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
8901	19639	32885	0.73	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22968	36187	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIf poly(ADP-ribose) 2 (Gtr2h2) genes, complete cds
10321	22968	36188	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIf poly(ADP-ribose) 2 (Gtr2h2) genes, complete cds
2671	15381	28119	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2671	15381	28120	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2924	15690	28334	2.87	9.4E+00	AB043795.1	NT	Mus musculus A13 gene for antithrombin, complete cds
7997	20692	33820	0.91	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8901	21592	34733	3.06	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IET) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.46	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5214	18022	30646	2.46	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
8330	21997		0.83	9.0E+00	P09241	SWISSPROT	RHODOPSIN
5945	18727	31685	5.55	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
8287	19060	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
8287	19060	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
430	13216	25861	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9365	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11122	23791		2	8.0E+00	P41820	SWISSPROT	BREIFELDIN A RESISTANCE PROTEIN
8051	20745		0.89	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	19931		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8259	20953	34090	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5711	18504	31426	2.66	7.4E+00	BF700517.1	EST_HUMAN	602128878F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8651	21343	34487	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15743	28390	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.58	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6931	19867	32713	0.71	7.2E+00	BE170900.1	EST_HUMAN	RCO-HT0613-200300-031-007 HT0613 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28186	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22151		8.63	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9882	22832	35729	3.37	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8181	20875	34011	1.92	6.9E+00	P35879	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
9031	21721		1.29	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10109	22757	35969	3.24	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5202	18010		0.72	6.8E+00	Q69028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6450	19218	32216	0.61	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
9974	22622	35827	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9974	22622	35828	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11073	23743		1.97	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9079	21768	34931	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10203	22851	36067	0.49	6.5E+00	BE866001.1	EST_HUMAN	601878435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960989 5'
9842	22294	35488	1.55	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10460	23106	36337	0.5	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
6938	19871	32717	1.46	6.0E+00	BE780163.1	EST_HUMAN	601498031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
9718	22367	35565	0.46	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1465000 nt position (6/7)
10411	23057	36274	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10411	23057	36275	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6428	19196	32183	7.32	5.9E+00	AF155142.1	NT	Mus musculus inbred lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3514	16270		0.99	5.8E+00	7061557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7061	19752	32816	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7061	19752	32617	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11458	23223	36458	2.59	5.6E+00	Q56278	SWISSPROT	LYCOPENE BETA CYCLASE
6157	18934	31901	0.69	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10678	23309		1.28	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11464	23221	36455	3.09	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
6830	19492	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
6830	19492	32515	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7789	20495		1.54	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8698	21380	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8698	21380	34535	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9936	22594	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9936	22594	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17496	30102	1.32	5.3E+00	L43128.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
7878	20673		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8882	21573		0.49	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11628	24225	37548	3.2	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
5377	18177		0.91	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186-009 HT0691 Homo sapiens cDNA
10271	22919		0.95	5.2E+00	AF248070.1	NT	Drosophila cratichneea R1B retrotransposable element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8861	21552	34698	0.9	5.1E+00	O18005	SWISSPROT	RHODOPSIN
9725	22376	35577	1.19	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6193	18969	31944	0.72	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.59	5.0E+00	BF308661.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22977	36197	3.07	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11280	23922	37214	8.95	5.0E+00	Z83890.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10132	22780		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NP-TS) gene, complete cds
4039	16784		10.88	4.8E+00	AF185255.1	NT	Eurice australis histone H3 (H3) gene, partial cds
8054	20748	33879	0.47	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8439	21131		5.28	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
283	13090	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
284	13090	25731	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875854F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4098716 5'
3268	16030	28679	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9085	21783	34948	1.18	4.6E+00	BE048437.1	EST_HUMAN	7e68g10.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:4280216 5'
9095	21783	34949	1.18	4.6E+00	BE048437.1	EST_HUMAN	KIAA0945 PROTEIN; contains element PTR5 repetitive element;
10287	22835		0.61	4.6E+00	AF240786.1	NT	7e68g10.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:4215284 5'
11054	23724		2.31	4.6E+00	D63999.1	NT	KIAA0945 PROTEIN; contains element PTR5 repetitive element;
11605	24204	37526	2.69	4.5E+00	AE001044.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11702	24353	37685	1.78	4.5E+00	BF068841.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 18/27, 2287280-2392728
3035	15801	28447	0.96	4.4E+00	BF530893.1	EST_HUMAN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3035	15901	28448	0.96	4.4E+00	BF530893.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
6109	18898		1.06	4.4E+00	X13414.1	NT	602072585F1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6027	18907		0.88	4.3E+00	AF056879.1	NT	602072585F1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
7338	20019	33097	2.03	4.3E+00	Y13402.1	NT	Murine I gene for MHC class IIa associated invariant chain
7515	20186	33280	0.65	4.3E+00	AE001222.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
10789	23453	36606	7.64	4.3E+00	AF240786.1	NT	Plasmodium falciparum R20R+var1 gene, exon 1
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	Treponema pallidum section 38 of 87 of the complete genome
5507	18305	31206	0.87	4.2E+00	P61826	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
6674	19591	32627	2.62	4.2E+00	P13983	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
6674	19591	32628	2.62	4.2E+00	P13983	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
8859	21550	34697	4.68	4.2E+00	AI080113.1	EST_HUMAN	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9818	22489	35672	1.06	4.2E+00	P31368	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
10049	22697		0.46	4.2E+00	P40888	SWISSPROT	wf67g03.x1 Soveres_NFL_I_G88C_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
5846	25079	31509	0.56	4.1E+00	O09185	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
5846	25079	31570	0.56	4.1E+00	O09185	SWISSPROT	HEXOSE TRANSPORTER HXT8
7012	19704	32780	0.84	4.1E+00	BE253688.1	EST_HUMAN	CELLULAR TUMOR ANTIGEN P53
7111	19798	32893	0.65	4.1E+00	BF247838.1	EST_HUMAN	CELLULAR TUMOR ANTIGEN P53
7559	20229	33332	8.73	4.1E+00	O23810	SWISSPROT	60110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:351534 5'
7681	20345		0.62	4.1E+00	AB041523.1	NT	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068758 5'
7683	20347	33459	4.32	4.1E+00	P28964	SWISSPROT	YY1 PROTEIN PRECURSOR
							Padinopecten yeissensis mRNA for calcineurin A, complete cds

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20347	33460	4.32	4.1E+00	P28984	SWISSPROT	GENE 88 PROTEIN
7817	20512	33638	2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive sdo LTR element in the RNU2 locus
9440	22118	35295	0.67	4.1E+00	P11263	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.46	4.1E+00	BF082425.1	EST_HUMAN	802247838F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333208 5'
10205	22853						CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10800	23483						(P27KIP1)
10892	23572						HYPOTHETICAL PROTEIN HVL1
3533	16289						801507510F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909051 5'
5372	19500	32524	0.77	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	19500	32525	0.77	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32524	0.75	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32525	0.75	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7089	19778	32843	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21464	34611	0.45	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
9843	22494	35695	0.44	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10085	22713	35931	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11537	24137	37444	2.27	4.0E+00	P07684	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3494	16290	28904	4.61	3.9E+00	X64518.1	NT	N. lactuca chitinase gene 50 for class I chitinase C
4287	17026		8.24	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5572	18369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-370500-028-h05 BN0070 Homo sapiens cDNA
5572	18369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-370500-028-h05 BN0070 Homo sapiens cDNA
6591	19354	32367	0.55	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RfRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6774	19518	32546	4.62	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	19946	33022	4.3	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8216	20910	34046	1.86	3.9E+00	X58865.1	NT	X-leucine mRNA for M4 muscarinic receptor
11365	23176	36403	3.3	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2635	15347		0.9	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6297	19070	32054	0.98	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
6673	19590	32626	0.66	3.8E+00	AJ493849.1	EST_HUMAN	q25107.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34161	1.1	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135-Human brain cDNA Homo sapiens cDNA clone 148
9694	22345		0.62	3.8E+00	AJ390981.1	NT	Streptococcus cricetus partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884
4001	16748	29379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7066	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8609	21301		0.55	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9076	21765	34928	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24067	37363	2.23	3.7E+00	BF669279.1	EST_HUMAN	802120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24067	37364	2.23	3.7E+00	BF669279.1	EST_HUMAN	802120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
579	13359	25986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4745	17477		1.06	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17983	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	801901868F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8450	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8450	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8543	21235	34378	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10759	23444		4.07	3.6E+00	M90785.1	NT	Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3241	18003	28652	1.1	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
5911	18995		1.17	3.5E+00	L28988.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6118	18996	31804	1.18	3.5E+00	R19745.1	EST_HUMAN	y940c08.t1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34940 5'
8383	21076		0.58	3.5E+00	P24657	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8930	21621	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86504.s1 Stritagens HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8930	21621	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86504.s1 Stritagens HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9393	22055	35227	0.96	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10417	23063	36283	0.46	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	26933	2.04	3.4E+00	AF254577.1	NT	Bos taurus RPB5d mRNA, complete cds
7261	18945	33021	2.04	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7601	20287	33374	0.89	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8577	21269		0.7	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROMK1, ROMK2, ROMK3, ROMK4, ROMK5, and ROMK6 (KCNJ1) gene, complete cds
8872	21662	34813	0.67	3.4E+00	AJ228042.1	NT	Homo sapiens 359 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9010	21700	34850	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM6SF2 gene for tetraspanin protein, exon 6
10164	22812	36030	2.97	3.4E+00	AF013187.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11519	24119	37429	1.89	3.4E+00	L77570.1	NT	Homo sapiens D1George syndrome critical region, centromeric end
5977	18759	31722	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5977	18759	31722	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7794	20489	33611	0.79	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
488	13273	25908	1.64	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4004	13273	25908	0.9	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4679	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5481	18280	31176	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-10PENE CYCLASE
5481	18280	31177	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-10PENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18988	31964	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6214	18988	31965	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7505	20178	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8928	21619		4.51	3.2E+00	P13081	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9430	22108	35283	0.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (ILD1) gene, complete cds
10041	22689	35907	2.03	3.2E+00	AB016081.2	NT	Oryza latipes OIGC8 gene for guarany cyclase C, complete cds
11946	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.46	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7287	19970	33047	0.93	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7627	20293		0.94	3.1E+00	AF303225.1	NT	<i>Bacillus alcalophilus</i> pectate lyase (pelE) gene, complete cds
7986	20881	33807	0.48	3.1E+00	P40885	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8500	21192	34333	4.36	3.1E+00	P40894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8500	21192	34334	4.36	3.1E+00	P40894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9168	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9796	22447	35652	0.59	3.1E+00	7524759	NT	<i>Chlorella vulgaris</i> chloroplast, complete genome
9888	22538		0.83	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 59.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10234	22882	36095	5.52	3.1E+00	P49365	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11440	23207		2.86	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11463	24006		3.28	3.1E+00	S50680.1	NT	retinoid acid nuclear receptor isoform beta 2 [nucleic acid, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
2842	15610	28259	1.09	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
6254	18060	30689	1.32	3.0E+00	X53096.1	NT	<i>S. aureus</i> gene: encoding <i>Sau981</i> DNA methyltransferase and <i>Sau961</i> restriction endonuclease
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	<i>Corynebacterium glutamicum</i> thrC gene for threonine synthase (EC 4.2.99.2)
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	<i>Corynebacterium glutamicum</i> thrC gene for threonine synthase (EC 4.2.99.2)
7056	19746		9.09	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7096	19785		0.8	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8605	21497		1.2	3.0E+00	X67838.1	NT	<i>B. napus</i> DNA for myosinase
10192	22840	36055	0.82	3.0E+00	Q58906	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10544	23240	36474	1.57	3.0E+00	Q10181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10931	23611	36890	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10931	23611	36890	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11578	24177	37492	2.72	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2004	14740	27464	2.28	2.9E+00	AE002225.2	NT	<i>Chlamydia pneumoniae</i> AF39, section 53 of 94 of the complete genome
6909	19470	32493	1.74	2.9E+00	Z36879.1	NT	<i>F. pingid</i> gdcA gene for P-protein of the glycine cleavage system
7110	19798	32861	5.21	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR



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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7110	19798	32962	5.21	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	6.94	2.9E+00	P46989	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7996	20691	33819	1.03	2.9E+00	BF344171.1	EST_HUMAN	60201741351 NC1 CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4183059 5'
1440	14187	20872	4.4	2.8E+00	AF196398.1	NT	Buxus harlandii methylase K (mefK) gene, partial cds; chloroplast gene for chloroplast product
1629	14375		2.74	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32968	6.72	2.8E+00	8393724	NT	Mus musculus andomuch (LOC83423), mRNA
9513	22106		0.54	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10598	19902	32968	1.32	2.8E+00	8393724	NT	Mus musculus andomuch (LOC83423), mRNA
224	13036	25672	13.51	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
224	13036	25673	13.51	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Pbx3), mRNA
5484	18263	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apoa polymorphism Kringle IV gene, exons 1 and 2
8045	20739		0.6	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8867	21558		1.83	2.7E+00	AL116499.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9332	20403	33519	0.73	2.7E+00	AW088191.1	EST_HUMAN	xc88e12x1 NC1 CGAP_Brm35 Homo sapiens cDNA clone IMAGE:2581374 3' similar to gb:M17733
10397	23043		1.75	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4626	17361	29694	5.15	2.6E+00	AF068749.1	NT	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5480	18259	31149	1.68	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5480	18259	31150	1.68	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5736	18528		0.59	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	25424		0.82	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7600	20209		0.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7958	20653	33778	1.13	2.6E+00	AJ132180.1	NT	Mus musculus iSH2-containing Inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7958	20653	33777	1.13	2.6E+00	AJ132180.1	NT	fabu bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
9557	22210	33395	2.83	2.6E+00	AL161540.2	NT	fabu bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
10253	22901		1.67	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10953	23630	36878	1.32	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12580	25304		3.17	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14195	26878	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TP), member 4 (ABCB4), mRNA
						NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1448	14195	26879	3.73	2.5E+00	AJ271844.1	NT	<i>Aspergillus nidulans</i> recQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31435	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6630	19392	32406	0.64	2.5E+00	D30062.1	NT	<i>Vibrio cholerae</i> ctxA gene and ctxB gene for cholera toxins, complete cds
7659	20323	33431	0.69	2.5E+00	AW049158.1	EST_HUMAN	QV4-FT0005-1: 0800-205-007 FT0005 Homo sapiens cDNA
7700	20363	33477	0.58	2.5E+00	4502802	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9001	21691	34941	1.53	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9752	22403	35608	0.67	2.5E+00	BE297758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
11943	24498		3.08	2.5E+00	AF289605.1	NT	<i>Mus musculus</i> IIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3012	15778	28428	1.13	2.4E+00	M24282.1	NT	Chicken alpha-2(I) collagen type VI mRNA, 3' end
4849	17579	30203	6.09	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5920	18705	31657	4.16	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7280	19984	33040	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120850F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	19984	33041	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120850F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8039	20734	33865	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8039	20734	33866	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8110	20804		2.63	2.4E+00	AE001488.1	NT	<i>Helicobacter pylori</i> , strain J99 section 47 of 132 of the complete genome
8549	21241		1.61	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-005 PT0004 Homo sapiens cDNA
8727	21419	34563	7.36	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9638	22598	35788	2.66	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9638	22598	35789	2.56	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10007	22655	35868	1.86	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10143	22791		6.55	2.4E+00	P09099	SWISSPROT	XYLOSE KINASE (XYLUKINASE)
10220	22806	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22808	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr6306.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10490	23136	36364	0.87	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11331	24022	37327	2.16	2.4E+00	AF158652.2	NT	<i>Fragaria x ananassa</i> cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1231	13980	26650	13.6	2.3E+00	Z46724.1	NT	<i>G. domesticus</i> artificial single chain antibody gene (L3)
4102	16845		1.35	2.3E+00	AJ401081.1	NT	<i>Bos taurus</i> partial cyto gene for cytochrome b

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5744	18536			2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7354	20035	33113	0.95	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Cat++ transporting, ubiquitous (Atp2a3), mRNA
7495	25425		2.47	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	3.07	2.3E+00	X80265.1	NT	M.musci dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9008	21698	34849	1.01	2.3E+00	5835317	NT	Polyporus ornaiipinnis mitochondrion, complete genome
9068	21757	34919	0.64	2.3E+00			ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10704	23395	36632	1.8	2.3E+00	Q11127	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11782	24373	37703	3.83	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11782	24373	37704	3.03	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24842	31099	3.03	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
3898	18746	29378	6.84	2.3E+00	BE995237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4278	17017	29844	0.95	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4278	17017	29845	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
			5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5258	18064	30692					SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5258	18064	30693	12.73	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5763	18554	31478			BE927220.1	EST_HUMAN	RC3-CT0254-3/0800-022-006 CT0254 Homo sapiens cDNA
5971	18753	31714	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-3/0800-022-006 CT0254 Homo sapiens cDNA
6261	19035	32010	9.84	2.2E+00	BE260383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6502	19287	32269	3.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6861	17938		3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7217	19902	32975	3.94	2.2E+00	AA594574.1	EST_HUMAN	nt95b02.s1 NC1_OGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7507	20178	33272	0.9	2.2E+00	AA137027.1	EST_HUMAN	ztr97704.11 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7589	20267	33365	19.2	2.2E+00	AA449012.1	EST_HUMAN	z05g10.11 Soles total_fetus_Nb21F8_9w Homo sapiens cDNA clone IMAGE:785834 5'
8001	20696	33823	0.72	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
							bb17h12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);

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8001	20698	33824	0.58	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9241	21920		1.02	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9408	25124		2.28	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
9853	22601	35804	1.1	2.2E+00	AI200373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NHP8609W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y01433 GLUTATHIONE PEROXIDASE (HUMAN);
9953	22601	35805	1.1	2.2E+00	AI280373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NHP8609W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y01433 GLUTATHIONE PEROXIDASE (HUMAN);
9998	22644	35858	2.68	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	23000	36217	3.11	2.2E+00	AF183418.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11418	23185	36415	3.47	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11616	24214	37539	5.89	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
556	15545	25967	8.3	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3575	16330		1.08	2.1E+00	AW449388.1	EST_HUMAN	U1-H-B13-ek1-e18-Q-JJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6041	18821		0.89	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6710	19625	32689	3.95	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-G-LYCOPROTEIN PRECURSOR (FETUIN-A)
6946	19428	32443	5.72	2.1E+00	N29575.1	EST_HUMAN	y08a10.s1 Soares_melanocyte_2NHPM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55854 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
8395	21088		1.97	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT21X2 Homo sapiens cDNA clone NT2RM2000671 5'
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1312	14060	26735	0.97	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na <sup>+</sup> /K <sup>+</sup> -ATPase beta 1 subunit mRNA, complete cds
1569	14316		2.61	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2145	14875	27609	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2145	14875	27610	5.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4080	16824	29450	2.2	2.0E+00	AW684498.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4080	16824	29451	2.2	2.0E+00	AW684498.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7449	20125		0.92	2.0E+00	P07568	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7923	20618	33745	3.17	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 46 min., complete cds
7923	20618	33746	3.17	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 46 min., complete cds
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 46 min., complete cds

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8620	21512	34956	3.15	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 Hm3 Homo sapiens cDNA clone s4000117B08
12481	25285	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.9E+00	6754389	NT	Mus musculus: nos1d1 1,4,5-triphosphate receptor 1 (ltp1), mRNA
5511	18309	31210	4.77	1.9E+00	6754389	NT	Mus musculus: nos1d1 1,4,5-triphosphate receptor 1 (ltp1), mRNA
6009	18790	31753	1.32	1.9E+00	BE969895.1	EST_HUMAN	601679638F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6556	19321		0.75	1.9E+00	AW1845689.1	EST_HUMAN	MRO-CT0063-C71098-002-g02 CT0063 Homo sapiens cDNA
6650	19412		2.46	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34190	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21249		2.94	1.9E+00	BF300206.1	EST_HUMAN	CM3-MT0114-C10800-323-h12 MT0114 Homo sapiens cDNA
8792	21484		1.33	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9530	22183	35367	0.59	1.9E+00	AA669125.1	EST_HUMAN	ab04a04.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10462	23108	36339	0.62	1.9E+00	AF248269.1	NT	Homo sapiens (p90-pro-p90 precursor protein gene, partial cds
3089	15854	28406	1.3	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3118	15853	28522	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3118	15853	28523	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5777	18598		1.91	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6013	18794	31757	1.32	1.8E+00	BF311989.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6305	19077		1.12	1.8E+00	BF683327.1	EST_HUMAN	602130470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4206272 5'
6641	19403	32418	1.64	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
6958	19440	32455	1.79	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8368	21061	34201	0.44	1.8E+00	P48634	SWISSPROT	ENDONUCLEASE
8368	21061	34202	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8753	21445	34593	1.98	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9073	21762	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	yh72608.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	QV0-O10030-070300-148-a03 OT0030 Homo sapiens cDNA

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9749	22400	35605	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10452	23098		0.63	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12276	25236		5.29	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
1086	13844	26502	2.21	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27734	2.29	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2372	15094	27833	2.56	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4426	17182	29792	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31223	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171298-127-e05 BT0282 Homo sapiens cDNA
5525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171298-127-e05 BT0282 Homo sapiens cDNA
5927	18711	31686	3.28	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7118	19806	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19806	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7753	20449	33573	0.91	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7932	20627	33755	1.13	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
7961	20656	33761	0.59	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214669 5'
8440	21132	34268	0.5	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus Interferon Inducible Mx protein (Ixx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8605	21297	34440	0.59	1.7E+00	X69063.1	NT	M.musculus Aric-1 mRNA for erythroid ankyrin
8605	21297	34441	0.59	1.7E+00	X69063.1	NT	M.musculus Aric-1 mRNA for erythroid ankyrin
9047	25123	34892	2.18	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9506	22159		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10071	22719		0.49	1.7E+00	AW953981.1	EST_HUMAN	EST365761 IMAGE resequences, MAGC Homo sapiens cDNA
11596	24195	37514	2.57	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12231	24694	31074	1.9	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1
12717	24990	30970	1.94	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element; qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1
2027	14762	27491	18.51	1.6E+00	AF199339.1	NT	repetitive element; Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2036	14771	27500	3.75	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2282	15007		1.24	1.6E+00	X08373.1	NT	B. napus gene encoding endo-polygalacturonase
2961	15727	28377	1.61	1.6E+00	W58428.1	EST_HUMAN	zid25701.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D28805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4011	16757		5.66	1.6E+00	BF570077.1	EST_HUMAN	6021860851 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	29882	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4319	17058	29883	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	AF075394.1	NT	Ureuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17669	30278	0.84	1.6E+00	AF075394.1	NT	Ureuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5737	18529	31450	2.16	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2701 gene, 3' end
5823	18612	31543	0.79	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-067800-145-E02 UT0073 Homo sapiens cDNA
6610	19373	32387	1.08	1.6E+00	AW29488.1	EST_HUMAN	UH-BI2-ahr-b-04-0-UI.s1 NCL CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7145	19832	32901	2.73	1.6E+00	BE987267.1	EST_HUMAN	RC0-CT0416-200700-032-c10 CT0416 Homo sapiens cDNA
7929	20624		1.19	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8277	20971	34112	3.28	1.6E+00	AJ287131.1	NT	Mus musculus SLL, MAP_17, CYP_a, SGL & CYP_b genes
8798	21490	34836	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8798	21490	34837	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21690	34810	0.47	1.6E+00	BE388331.1	EST_HUMAN	601283025F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9360	25121	33549	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9360	25121	33550	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9487	22140		0.66	1.6E+00	AF043486.1	NT	Thermococcus acter ethanolicus D-xylose-binding protein (XylF) gene, complete cds
9634	22266	35480	1.32	1.6E+00	T41290.1	EST_HUMAN	phib6_18/1TV Outward AU-primered hncDNA library Homo sapiens cDNA clone phib6_18/1TV
10047	22695	35911	0.5	1.6E+00	AF121981.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zhc finger protein (DNZ1) genes, complete cds
10085	22733	35947	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-030200-100-407 LT0016 Homo sapiens cDNA
10085	22733	35948	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-030200-100-407 LT0016 Homo sapiens cDNA
10242	22890	36102	0.47	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	36365	0.45	1.6E+00	AF162084.1	NT	Glucose pleocoglycol beta-tubulin 2 (tub2) gene, partial cds



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10670	23361	36602	1.95	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10728	23416	36657	1.27	1.6E+00	AA216387.1	EST_HUMAN	nc18002.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008267 similar to contains element MER4 repetitive element;
10747	18612	31643	5.27	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
11705	24300	37628	3.48	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12859	26476	5.31	1.5E+00	U63449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25674	2.2	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AFR39, section 32 of 94 of the complete genome
606	13384		2.03	1.5E+00		NT	Mus musculus: a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2519	16235	27975	2	1.5E+00	6678350	NT	Mus musculus: T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3388	16127	28785	0.72	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5642	18437	31350	0.83	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.;
5642	18437	31351	0.83	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.;
6312	19083	32068	3.02	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7060	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7060	19751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7245	19630	33006	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak28f10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7463	20165	33257	0.76	1.5E+00	AI003254.1	EST_HUMAN	ar07b11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684863 3' similar to gb:S85836 SEROTRANSFERRIN PRECURSOR (HUMAN);
7727	20390		0.84	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8021	20716	33848	0.89	1.5E+00	BE887446.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02738.1	NT	Mouse germline IgM chain gene, mu-delta region
8914	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens KGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34876	0.46	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9383	22045	35217	0.84	1.5E+00	R81928.1	EST_HUMAN	YC38101.r1 Soares placenta Nk2-IP Homo sapiens cDNA clone IMAGE:147697 5'
9635	22186	35374	1.39	1.5E+00	AW375997.1	EST_HUMAN	QV3-CT0192.2;J01099-008-d09 CT0192 Homo sapiens cDNA
9760	22411	35618	6.39	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183885 5'
10096	22744	35958	1.66	1.5E+00	AA017689.1	EST_HUMAN	za38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10096	22744	35559	1.66	1.5E+00	AA017689.1	EST_HUMAN	z38g06.r1 Soes retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11375	23982	37282	4.46	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547P243 3'
11530	24130		6.55	1.5E+00	X07390.1	NT	Malze mitochondrial RNA-Ser gene and RNA-Phe pseudogene
11629	24226	37549	2.1	1.5E+00	A1400798.1	EST_HUMAN	ig94d09.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2118433 3'
11629	24226	37550	2.1	1.5E+00	A1400798.1	EST_HUMAN	ig94d09.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2118433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12445	24815		3.38	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
28	12656	25472	2.76	1.4E+00	7881685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	12656	25473	2.76	1.4E+00	7881685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2333	15057		6.92	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2675	15384	28125	2.21	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2776	15481	28221	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2776	15481	28222	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4545	17280		1.81	1.4E+00	BF081547.1	EST_HUMAN	802156887F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287556 5'
5288	18093	30754	1.61	1.4E+00	AW054976.1	EST_HUMAN	wf45g07.x1 NC1 CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
6441	18240		6.57	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6186	18963	31936	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6318	19089	32074	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	19089	32075	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
7186	19872	32946	2.07	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7201	19887	32962	1.17	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NC1 CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7258	19942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7258	19942	33019	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8233	20927		0.88	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8991	21681	34829	1.73	1.4E+00	R20459.1	EST_HUMAN	yg33f12.r1 Soeris infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9097	21785	34951	4.85	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301298-012405 BT0313 Homo sapiens cDNA
9131	21819	34985	0.61	1.4E+00	AF134844.1	NT	Scoloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10108	22756	35688	0.79	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	22789	36015	0.61	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT0198-281099-008-C04 HT0198 Homo sapiens cDNA
10151	22799	36016	0.61	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10424	23070	36291	1.08	1.4E+00	D69441.1	NT	Pandorina colonensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	36292	1.08	1.4E+00	D69441.1	NT	Pandorina colonensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23675	36931	1.34	1.4E+00	AA195528.1	EST_HUMAN	Z36609.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element
11188	23853	37139	6.16	1.4E+00	AB008882.1	NT	MER22 repetitive element;
11381	23988	37288	4.42	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APECE2 mRNA for AIRE-1, complete cds
11381	23988	37289	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.48	1.4E+00	U30790.1	NT	601655184R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37358	3.48	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. reidi guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12079	25256		1.48	1.4E+00	AL161500.2	NT	Pneumocystis carinii f. sp. reidi guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
567	13339		1.81	1.3E+00	Z73840.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
882	13851	26320	3.42	1.3E+00	AJ271192.1	NT	M.mucoso gene encoding 4-Dihydroxyethyl-trispartate dehydrogenase
1107	13864		20.26	1.3E+00	Y19213.1	NT	Cartharellus sp. partial 2S rRNA gene, isolate Tibet
1274	14024	26802	13.71	1.3E+00	4507988	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
1274	14024	26803	13.71	1.3E+00	4507988	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1605	14351		2.27	1.3E+00	AE002338.2	NT	Coat lectyne-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
2239	14987		1	1.3E+00	AB030447.1	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2405	15126	27862	1.27	1.3E+00	P25391	SWISSPROT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2553	15268		1.75	1.3E+00	BE968735.2	EST_HUMAN	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2940	15705	28354	0.73	1.3E+00	6755621	NT	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915845 3'
3584	16339	28964	0.89	1.3E+00	AF018494.1	NT	Mus musculus alpha-spectrin 1, erythrocyte (Spn1), mRNA
5427	18226	30638	1.09	1.3E+00	P19732	SWISSPROT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane enhancer protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase
5622	18418	31330	0.6	1.3E+00	M27138.1	NT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL-2-MONOOXYGENASE P3 COMPONENT)
5963	18560	31590	0.81	1.3E+00	BF663825.1	EST_HUMAN	Human estradiol 17 beta-dehydrogenase gene, complete cds
5928	18712	31687	7.57	1.3E+00	AW362834.1	EST_HUMAN	602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5'
							PMO-CT0289-231189-004-f08 CT0289 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5928	18712	31668	7.57	1.3E+00	AW32834.1	EST_HUMAN	PMO-CT0288-2i1199-004-f08 CT0288 Homo sapiens cDNA
6323	19083	32081	1.34	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6652	19414		0.75	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6739	19573	32806	0.62	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (TGA5) mRNA, partial cds
6854	19554	32584	1.17	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7000	19692	32743	0.81	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0850 P-ediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7358	20039		1.01	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8197	20891	33117	1.28	1.3E+00	AJ009812.1	NT	Sus scrofa pig gene
8346	21039	34176	2.78	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3868195 3'
8459	21151	34294	0.86	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303		1.78	1.3E+00	8910247	NT	Homo sapiens G-004 protein (GLO04), mRNA
8689	21381	34525	0.79	1.3E+00	A827629.1	EST_HUMAN	w055a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9415	22063		5.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.56	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9424	22102	35274	2.56	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9524	22177	35361	0.96	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9569	22222	35407	1.56	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMMAN)
9651	22303	35498	1.14	1.3E+00	A927629.1	EST_HUMAN	w055a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9726	22377	35578	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-Invt1 chromosomal inversion junction DNA
9726	22377	35579	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-Invt1 chromosomal inversion junction DNA
9766	22417	35624	4.53	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3868195 3'
9826	22477		0.48	1.3E+00	A1559644.1	EST_HUMAN	lq77a12.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723
10050	22698	35913	0.46	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10050	22698	35914	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	35974	1.62	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10130	22778	35991	1.35	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10483	23128		0.82	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C102
10511	23157	36383	0.45	1.3E+00	A1990846.1	EST_HUMAN	w032a10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TR08_HUMAN
10592	23286		4.6	1.3E+00	Q14117	SWISSPROT	Q16881 THIOREDOXIN REDUCTASE; DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	36744	1.93	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10846	23528	36772	2.01	1.3E+00	Z18892.2	NT	Mus musculus <i>leemln</i> gene
11307	23686		1.8	1.3E+00	AW274791.1	EST_HUMAN	xp0903.x1 NC1_CGAP_HND Homo sapiens cDNA clone IMAGE:2739868 3'
11527	24127	37433	3.21	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z98882.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
12210	24775		2.64	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNU12) gene, complete cds
12388	24780	31035	6.3	1.3E+00	BF346043.1	EST_HUMAN	602023185F1 NC1_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158452 5'
12397	25153		2.73	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	24848		2.15	1.3E+00	AF187035.1	NT	Slumira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
635	13414	26050	11.05	1.2E+00	AA076246.1	EST_HUMAN	Z12208.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431635 3'
804	13576	26239	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26240	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13578	26241	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13627		1.36	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1136	13693	26554	5.64	1.2E+00	AF080245.2	NT	Elaeis oleifera e-acyltransferase synthase mRNA, complete cds
1183	13935	26600	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26601	1.26	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15973	28512	1.24	1.2E+00	AB020981.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15928	28573	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15928	28574	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3280	18041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3698	18452	29091	6.69	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3957	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4266	16110	28768	1.11	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4438	17174		1.57	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4487	17222	29850	0.96	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17258	29862	1.89	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4548	17283		6.43	1.2E+00	Y09200.1	NT	T. pinatum chloroplast rbcL gene, partial
5351	18154	30836	1.1	1.2E+00	U20780.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5467	18296	31158	1.91	1.2E+00	AW813276.1	EST_HUMAN	MR3-S10181-140200-013-c05 S10181 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6080	18840	31801	2.51	1.2E+00	X74885.1	NT	Dhydel a1 repeat cluster DNA, fragment D
6119	18897	31865	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6198	18974	31951	1.54	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6198	18974	31952	1.54	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6241	19015	31989	39.54	1.2E+00	AA759254.1	EST_HUMAN	sh84g12.s1 Scarsa_testis_NHT Homo sapiens cDNA clone 1322374.3'
6342	19112	32101	0.55	1.2E+00	N33295.1	EST_HUMAN	yy39b12.s1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273598 3' similar to gbJ87935HUMALU472 Human carcinoma cell-derived Alu RNA transcript (rRNA); gbJ04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6408	19177	32175	0.88	1.2E+00	P17671	SWISSPROT	ECODYSONE-INDUCIBLE PROTEIN E75-A
6412	19180	32179	2.06	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-005 ST0191 Homo sapiens cDNA
6815	19476	32498	1.17	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
6829	19490	32512	3.11	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7153	19840		0.94	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7282	25109	33044	4.86	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cDNA Homo sapiens cDNA clone cAAAFH03 5'
7550	20220	33323	2.49	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
7603	20269	33376	0.56	1.2E+00	J05218.1	NT	Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
7715	20379	33492	0.56	1.2E+00	BE787848.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8467	21159	34302	3.32	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8561	21253	34391	0.88	1.2E+00	P38427	SWISSPROT	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
8775	21487		0.51	1.2E+00	7708271	NT	GLUCOSYLTRANSFERASE)
8923	21614	34758	1.87	1.2E+00	AW377210.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9138	21826	34991	0.5	1.2E+00	H48569.1	EST_HUMAN	MR2-CT0222-101099-001-e07 CT0222 Homo sapiens cDNA
9298	21965	35138	3.75	1.2E+00	Z32850.1	NT	yc80a06.r1 Scirres fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202068 6'
9505	22168	35339	1.81	1.2E+00	D11745.1	EST_HUMAN	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9631	22482	35884	2.86	1.2E+00	X58832.1	NT	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01.e01
10224	22872		0.73	1.2E+00	AB006666.1	NT	H.sapiens ENC3 gene for muscle specific enolase
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	Homo sapiens lidofo gene, exon 1
11357	24045		10.82	1.2E+00	BE160761.1	EST_HUMAN	PM0-ST0284-16169-001-d01 ST0284 Homo sapiens cDNA
11435	23202	36434	4.36	1.2E+00	U50147.1	NT	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
12179	25227	30817	17.08	1.2E+00	AL163203.2	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12199	24687		2.8	1.2E+00	AP001515.1	NT	Homo sapiens chromosome 21 segment HS21C003
451	13237	25876	1.53	1.1E+00	D86980.1	NT	Bacillus halodurans genomic DNA, section 9/14
1757	14499	27200	1.33	1.1E+00	AW695393.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
1892	14629	27339	0.98	1.1E+00	AW575889.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
							UIHF-BR0p-aj1-4-02-0-U1.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3480	16238	28892	1.11	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	16322	28970	1.01	1.1E+00	AB080380.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359481 3' similar to
3707	16460	29098	1.05	1.1E+00	AEO03886.1	NT	SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;
3707	16460	29099	1.05	1.1E+00	AEO03886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3798	16550		1.02	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4190	16931		5.69	1.1E+00	5835331	NT	H. paratuberculosis hphIM(A), hphIM(C), hphIR and menB genes
4634	17369		0.81	1.1E+00	U34992.1	NT	R. uniconis complete mitochondrial genome
4934	17662	30272	3.45	1.1E+00	U18406.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
4935	17663	30273	1.05	1.1E+00	AJ271740.1	NT	African swine fever virus, complete genome
5128	17847	30464	1.07	1.1E+00	6980080	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5224	18031	30657	1.39	1.1E+00	6978630	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5528	18324	31225	15.75	1.1E+00	BE960184.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5545	18342	31250	1.2	1.1E+00	AI138592.1	EST_HUMAN	801652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6001	18782	31743	1.1	1.1E+00	11419739	NT	qd86c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6181	18958	31932	0.62	1.1E+00	AF197861.1	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6313	19084	32060	0.82	1.1E+00	R08037.1	EST_HUMAN	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6616	19379	32394	0.72	1.1E+00	AJ404004.1	NT	ye98c03.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124924 5'
7155	19842		0.98	1.1E+00	AF101091.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7198	19882	32956	0.72	1.1E+00	X55081.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7389	20068	33146	2.18	1.1E+00	Z72838.1	NT	Maize mRNA for endoplasmic reticulum (2-phospho-D-glycerate hydrolase)
7389	20068	33147	2.18	1.1E+00	Z72838.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7411	20086	33172	8.94	1.1E+00	AL161588.2	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7480	25115	33247	0.8	1.1E+00	11907980	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8032	20727	33860	3.01	1.1E+00	BF063996.1	EST_HUMAN	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8120	20814	33950	0.84	1.1E+00	AJ478339.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
8638	21328	34471	0.71	1.1E+00	AB003088.1	NT	hm3ah11.x1 NCJ_CGAP_K411 Homo sapiens cDNA clone IMAGE:2160549 3'
8714	21406	34549	0.75	1.1E+00	S80750.1	NT	Acetabularia caliculata mitochondrial COX-like gene
							VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	21516	34661	0.45	1.1E+00	A1079946.1	EST_HUMAN	oz34f05.x1 Sources_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		0.69	1.1E+00	BE394876.1	EST_HUMAN	001276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35365	0.53	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Simx gene)
9580	22233		1.2	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9672	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22383	35585	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
9837	22488	35600	4.59	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36260	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23150	36375	0.73	1.1E+00	A1878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518282 5' similar to gb:D10522
10547	23243	36478	2.25	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN);
10606	23300		3.1	1.1E+00	AF068842.1	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
11023	23685	36859	1.28	1.1E+00	11439598	NT	Klebsorridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11028	23698	36861	1.58	1.1E+00	L16877.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11042	17901		5.23	1.1E+00	8022673	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11048	23718	36888	3.88	1.1E+00	AF012862.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36888	3.88	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11328	24019	37323	4.58	1.1E+00	A1806699.1	EST_HUMAN	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11561	24160	37470	1.63	1.1E+00	D89501.1	NT	wf76e11.x1 Sources_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11561	24160	37471	1.63	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12153	24638		3.66	1.1E+00	P07866	SWISSPROT	Human PBI gene, complete cds
12250	24697	31078	1.93	1.1E+00	AF216898.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12378	25225		2.09	1.1E+00	AF234169.1	NT	Taenla solium immunogenic protein Te76 mRNA, partial cds
12388	25200		1.44	1.1E+00	8393198	NT	Dictyostelium discoideum isopenicillin pyrophosphate isomerase (DipI) mRNA, complete cds
97	12923		2.46	1.0E+00	U23808.1	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Crp), mRNA
111	12932	25569	0.73	1.0E+00	D88425.1	NT	Xenopus laevis rhodopsin gene, complete cds
409	13194		2.25	1.0E+00	AB021694.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
562	13344	25971	1.2	1.0E+00	AJ251690.1	NT	Marchantia polymorpha genes for 28S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 28S rRNA
662	13438	26079	4.38	1.0E+00	AL163218.2	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
							Homo sapiens chromosome 21 segment HS21C018

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
663	13439		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti nuclein-like protein MUC1 mRNA, complete cds
1305	15567		3.03	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1751	14483	27183	0.93	1.0E+00	AB008531.1	NT	Plasmodium falciparum RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2489	15206	27947	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2489	15208	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2878	15645	28287	3.82	1.0E+00	P24006	SWISSPROT	3-OXO-5-ALPHA-A-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15645	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-A-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2967	15733		1.17	1.0E+00	Q14228	SWISSPROT	HYPOHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I
3194	15957	28809	1.24	1.0E+00	AA628463.1	EST_HUMAN	af28908.s1 Sources: total_fetus_Nb2HF8_pw Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA208.3 CE04204; contains element MER22 MER22 repetitive element;
3585	12923		1.24	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3669	16422	28063	1.04	1.0E+00	AJ23816.1	NT	Agaricus bisporus mRNA for tyrosinase
4050	16795	29424	0.76	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4242	16983		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4954	17680		0.93	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
4875	17698	30306	0.74	1.0E+00	AF092505.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 8 (Dpp8) gene, partial cds; and proctinal Rump white inversion breakpoint
5200	18008	30829	3.53	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551	31472	4.97	1.0E+00	AF248094.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5769	18551	31473	4.97	1.0E+00	AF248094.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5997	18654	31995	1.53	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA J FCA config fragment No. 6
6024	18804	31785	4.7	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	UIH-B13-abx-4-19-Q-JJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088969 3'
6397	19166	32166	1.96	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6447	19215	32213	0.91	1.0E+00	AF104698.1	NT	Homo sapiens cell cycle protein (PA204) gene, exons 2 through 5
6534	19300		1.06	1.0E+00	P48606	SWISSPROT	SRB-11 PROTEIN
6678	19598	32634	1.33	1.0E+00	Y11204.1	NT	V. carteri gene encoding valatopsin



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7038	19730	32788	1.09	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058		9.29	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7611	20277	33385	1.56	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7626	20282	33401	5.26	1.0E+00	AA775191.1	EST_HUMAN	ec78608.s1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
7861	20556	33681	1.36	1.0E+00	BE88267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7861	20556	33682	1.36	1.0E+00	BE88267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8041	17680		1.19	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
							PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34079	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34080	2.02	1.0E+00	Q02207	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8376	21089		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8408	21101	34237	0.5	1.0E+00	Q875T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8408	21101	34238	0.5	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8436	25122		2.34	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0228-111099-011-e06 HT0228 Homo sapiens cDNA
8476	21168	34912	0.88	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8625	21317	34459	1.27	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9171	21841	35006	2.43	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9510	22163	35345	1.83	1.0E+00	AV889554.1	EST_HUMAN	AV889554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9516	22168	35351	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
9516	22169	35352	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9753	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9753	22404	35610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35875	0.71	1.0E+00	5174562	NT	Homo sapiens I/HC binding factor, beta (MHCBBF) mRNA
10012	22660	35876	0.71	1.0E+00	5174562	NT	Homo sapiens I/HC binding factor, beta (MHCBBF) mRNA
10104	22752	35958	0.81	1.0E+00	A077920.1	EST_HUMAN	oy15d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665801 3'
10225	22873	36085	4.36	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM1 Homo sapiens cDNA clone BMFAWG04 5'
10375	23021	36237	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.t1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10375	23021	36238	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.t1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10407	23053	36270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10693	23573	36823	4.57	1.0E+00	S90825.1	NT	PBR1-proline-rich protein (intron 3) [human, Genomic, 898 nt]
11025	23697	36960	1.49	1.0E+00	AA701494.1	EST_HUMAN	zf63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element, contains element MER38 repetitive element ;
11522	24122		1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18006	30629	1.55	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11838	24422	37763	12.28	1.0E+00	Q60019	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11868	24452	37794	1.38	1.0E+00	8626187	NT	Human adenovirus type 5, complete genome
12049	24568		3.01	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772		2.92	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAG resequences, MAGN Homo sapiens cDNA
2643	15363	28097	1.19	9.8E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3591	16346		0.97	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5547	18344	31253	10.09	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
5779	18570	31498	0.93	9.9E-01	Q06032	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9160	21830		1.37	9.9E-01	U65667.1	NT	Lycopodium obscurum putative M1 copy 1 nematode-resistance gene
9455	22005		2.18	9.9E-01	Q26642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10614	23308	36547	2.37	9.9E-01	AJ005028.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase ritk8
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. subter)
11592	24191	37509	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. subter)
510	13284	25929	1.14	9.8E-01	P22597	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	15020		1.21	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	15509		1.01	9.8E-01	AF174844.1	NT	Xenopus laevis ac GTPase mRNA, complete cds
3781	16533	29171	0.92	9.8E-01	O67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV)
7099	19788	32852	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JH963 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JH963

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7099	19788	32853	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33315	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7545	20215	33317	1.15	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8619	21311	34453	0.91	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10335	22983		1.13	9.8E-01	AA825585.1	EST_HUMAN	cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23586	36842	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33560750 5'
10916	23586	36843	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33560750 5'
11764	24355	37688	1.57	9.8E-01	A1680876.1	EST_HUMAN	b42c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12256	24702		1.56	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7058	19749	32812	2.28	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8401	21094	34230	1.88	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8407	21100	34236	1.3	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11123	23792		3.64	9.7E-01	BF511209.1	EST_HUMAN	UIH-B14-eol-e-17-Q-UI.at NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
4425	17161	29791	1.5	9.6E-01	AW798674.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5667	18482	31376	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5667	18482	31377	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6648	19410	32424	0.61	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8291	20985		2.33	9.6E-01	X95275.1	NT	P.falciparum complete gene map of plasid-like DNA (IR-A)
8750	21442	34589	0.59	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11503	24104	37416	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG08 5'
11503	24104	37417	3.47	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG08 5'
11952	24505		1.92	9.6E-01	11421722	NT	Homo sapiens centromeres protein 2 (CEP2), mRNA
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2480	15198	27938	1.05	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2673	15392	28122	0.97	9.5E-01	Q02934	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I)
3762	16514	29150	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3762	16514	29151	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8899	21800	34730	0.69	9.5E-01	A1190162.1	EST_HUMAN	q657407.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1793581 3'
9003	21603	34843	1.05	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-502 CT0295 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11209	23872	37159	1.88	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11429	23196	36427	2.42	9.5E-01	AW283799.1	EST_HUMAN	UI-H-B12-4hp-f-13-Q-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11795	24385	37718	1.55	9.5E-01	T67204.1	EST_HUMAN	ya53d04.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:66831 3'
3196	15959		3.33	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3212	15975		2.06	9.4E-01	AF080595.1	NT	Plimphella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34806	0.87	9.4E-01	M60724.1	NT	Human Fe-gamma-receptor IIA (FCGR2A) gene, exon 4
12202	24670		1.92	9.4E-01	BE781251.1	EST_HUMAN	601469703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868929 5'
12557	25219		1.79	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1728	14466		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytenoyl-CoA hydroxylase (PHYH) gene, exon 5
2640	15351	28095	1.98	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0603-Z71199-011-B01 BT0503 Homo sapiens cDNA
4015	16761	29388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	29389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5505	18303	31204	1.56	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18398	31298	3.98	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7666	20691	33785	1.05	9.3E-01	AA847040.1	EST_HUMAN	oe08b03.s1 NCI CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8835	21527	34673	0.95	9.3E-01	AL161834.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24970		3.12	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
12802	25049		1.48	9.3E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
3233	15995	28648	2.93	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4822	17653		0.97	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5631	18428		1.15	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5898	18683	31631	7.36	9.2E-01	BF037696.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6637	19302	32308	0.61	9.2E-01	M84703.1	NT	N.crassa val1-RNA synthetase (cyl-20/un-3) gene
9600	22213	35389	0.92	9.2E-01	AL161655.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9648	22300	35496	1.07	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22862	36178	1.9	9.2E-01	BF693251.1	EST_HUMAN	7658a06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10543	23239	36473	1.63	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-LIBIQUINONE OXIDOREDUCTASE CHAIN 5;
							601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24316	37639	1.79	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1821	14388	27057	1.88	9.1E-01	T98675.1	EST_HUMAN	y528701.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2120	14851		2.78	9.1E-01	8923056	NT	Alu repetitive element; Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15983	28914	1.15	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3200	15983	28915	1.15	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6075	18954	31821	1.28	9.1E-01	L36033.1	NT	HUMAN pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6413	19181	32180	3.53	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7475	20148	33241	17.62	9.1E-01	AA806023.1	EST_HUMAN	cd71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7637	20302	33410	2.34	9.1E-01	U72695.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10075	22723	35640	0.45	9.1E-01	P38432	SWISSPROT	P80-COLLIN
12281	25294		27.98	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4346	17085	29714	2.08	9.0E-01	AF090810.1	NT	Homo sapiens neuradin III-alpha gene, partial cds
7291	19874	33052	0.72	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7321	20004		1.18	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9249	21928	35100	0.49	9.0E-01	AF086761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
5810	18408	31318	2.68	8.9E-01	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6154	18931		1.38	8.9E-01	X80698.1	NT	Rabbit MHC fragment RLA-DF DNA
8325	21018	34154	0.71	8.9E-01	AF259967.1	NT	Olfraona nana cytochrome-c oxidase subunit 1 (cox1) gene, partial cds; mitochondrial gene for mitochondrial product
11787	24377	37707	2.51	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 80 of 229 of the complete genome
12138	24627		2.86	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
12762	28343		2.51	8.9E-01	A1150836.1	EST_HUMAN	gb64408.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1704879 3'
4505	17240	29873	3.82	8.8E-01	O28350	SWISSPROT	PUTATIVE F42I-DEPENDENT NADP REDUCTASE
5289	18094	30755	0.67	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22779	35992	0.83	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23690	36953	4.96	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11968	25382		1.8	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576693-1719843
452	13238	25877	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens A1-binding transcription factor 1 (ATBF1), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15644	28286	5.05	8.7E-01	AA595863.1	EST_HUMAN	nm05f11.s1 NC1_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
4946	17673		3.17	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5102	17820		0.97	8.7E-01	AJ288085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
7939	20634	33781	0.82	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120600-013-c07 NN0057 Homo sapiens cDNA
8828	21520	34685	0.89	8.7E-01	AJ239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
8828	21520	34696	0.89	8.7E-01	AJ239456.1	EST_HUMAN	qh36e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9838	22290	35483	1.57	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10202	22850	36085	0.81	8.7E-01	BF570190.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10202	22850	36098	0.81	8.7E-01	BF570190.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10735	23422	36885	5.25	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	6.47	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
462	13247		1.79	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
838	13608	26279	3.45	8.6E-01	W68089.1	EST_HUMAN	zid44e03.r1 Soares_fetal_heart_NH19W Homo sapiens cDNA clone IMAGE:343516 5'
2268	14994	27733	0.96	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatois) polypeptide 1 (CYP27A1b) mRNA
3608	16361	29003	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3782	16534	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster metlin (Dmetlin) mRNA, complete cds
5808	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5808	18597	31526	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6609	18372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6609	18372	32386	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104		0.76	8.6E-01	AE000591.1	NT	Helicobacter pylori 26895 section 68 of 134 of the complete genome
7828	20523		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7941	20636	33763	0.55	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapse response mediator protein (CRMP) mRNA, complete cds
9585	22238		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12518	25144		1.35	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6628	19388	32401	0.95	8.6E-01	AF166214.1	NT	Bacteriophage X3, complete genome
7425	20102	33189	2.51	8.6E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8317	21010	34147	0.78	8.6E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8317	21010	34148	0.78	8.6E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.6E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22898	36105	1.17	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10248	22898	36106	1.17	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12278	25298		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
4702	17436	30067	0.73	8.4E-01	AF083975.2	NT	Fowl adenovirus 1, complete genome
5406	25098	30910	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25098	30911	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF051142.1	NT	Maneestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
9658	22508		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
724	13498	26151	2.8	8.3E-01	M33437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	15858	28497	2.99	8.3E-01	AL161608.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3790	18542	29177	0.79	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3993	16741	28375	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17995	30511	2.41	8.3E-01	AL161640.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9588	22221		4.51	8.3E-01	A1791952.1	EST_HUMAN	repetitive element
10010	22658	35872	1.27	8.3E-01	AF098070.1	NT	Drosophila melanogaster L11 homolog mRNA, complete cds
10118	22768	35978	3.46	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10572	23267	36505	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10590	23284		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	23935	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, disadenosine triphosphate hydrolase (FHIT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145689.1	NT	Mus musculus trophinin (Tnm) gene, complete cds
2686	15395		1.06	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
6678	19593	32631	0.75	8.2E-01	AJ010142.1	NT	Amarilla muscaria mRNA for SCII25 protein
6797	19541	32589	3.49	8.2E-01	AW379433.1	EST_HUMAN	GM4-HIT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7169	25106	32928	4.74	8.2E-01	Z12128.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8343	21036	34173	0.59	8.2E-01	BE263145.1	EST_HUMAN	60114485F2 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9824	22572	35770	0.65	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9859	22807	35812	1.37	8.2E-01	AF052859.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10123	22771	35985	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35986	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10283	22831	36145	3.65	8.2E-01	Q9J70	SWISSPROT	MCKUSICK-KALIFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22931	36146	3.65	8.2E-01	Q9J70	SWISSPROT	MCKUSICK-KALIFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11641	24238	37562	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328	37652	6.38	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	8.02	8.2E-01	H87398.1	EST_HUMAN	yw14002.1 Soares_placenta_860weeks_2Nblp860W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12298	24723	31054	2.37	8.2E-01	AJ01261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2762	15467		1.08	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207	28857	3.08	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3451	16207	28858	3.08	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
4863	17592		0.74	8.1E-01	AF020634.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6223	18997	31973	0.84	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2(XI) chain (COL11A2) gene, partial cds
6526	19292	32295	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6526	19292	32296	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7229	19914	32987	0.78	8.1E-01	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7412	20089	33173	0.65	8.1E-01	O47477	SWISSPROT	CYTOSOLIC PROTEIN
7811	20506	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nack) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
7811	20506	33629	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nack) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gpr) gene, partial cds
8507	21199	34344	0.93	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21199	34345	0.93	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8868	21390	34507	1.08	8.1E-01	AW242647.1	EST_HUMAN	xb01h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW1LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.b1 PTR5.repetitive element;
10025	22673	35888	0.7	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10311	22888	36174	0.5	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
11464	24067	37374	2.63	8.1E-01	BE938598.1	EST_HUMAN	EST(C-ONE C-ONE11)
11464	24067	37375	2.63	8.1E-01	BE938598.1	EST_HUMAN	RC0-TN0080-22:800-025-d10 TN0080 Homo sapiens cDNA
12022	24550	31110	1.57	8.1E-01	AE001711.1	NT	RC0-TN0080-22:800-025-d10 TN0080 Homo sapiens cDNA
172	12985		3.49	8.0E-01	AJ271510.1	NT	Thermoboga maritima section 23 of 136 of the complete genome Staphylococcus aureus partial pla gene for phosphatase allele 15



Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus: protease (prosome, macropain) 28 subunit, alpha (Psmc1), mRNA
2029	14764		1.91	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NC1 CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215091 5'
3075	15841	28484	1.2	8.0E-01	AF127897.1	NT	Salmonella typhimurium: defecatory receptor (SBO27) gene, partial cds
3307	16037	28716	1.35	8.0E-01	AB009183.1	NT	Mus musculus gene for orofacial glycoprotein, complete cds
3680	16443		1.62	8.0E-01	AL192758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4496	17232	29862	8.05	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7889	20584		2.25	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8423	21116	34254	0.98	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10878	23556	36803	2.78	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN
441	13227	25870	1.18	7.9E-01	D11478.1	NT	Lymnaea disper nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	13473		1.14	7.9E-01	AE002130.1	NT	Unsplesma urealyticum section 31 of 59 of the complete genome
1600	14346		22.68	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
1662	14398		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2259	14966	27726	5.86	7.9E-01	AB004816.1	NT	Onchocerca cuticulus mRNA for mitsugumih29, complete cds
2260	14987	27727	2.4	7.9E-01	AF130459.1	NT	Danio rerio Tnp4-associated protein Tap1A (tap1A) mRNA, complete cds
3506	16262	28916	3.01	7.9E-01	AF228694.1	NT	Gallus gallus SOX3 transcription factor (SOX3) mRNA, complete cds
4268	17008		0.85	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4572	17307	29935	1.13	7.9E-01	6763745	NT	Mus musculus enibigh (Emb), mRNA
4572	17307	29836	1.13	7.9E-01	6763745	NT	Mus musculus enibigh (Emb), mRNA
6252	19028	32000	0.67	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33831	2.79	7.9E-01	X00998.1	NT	P. sativum GR gene
9447	22124	36304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vsg3M-B) mRNA, partial cds
9949	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9981	22639	35849	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10408	23054	36271	1.94	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10516	23162	36389	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10929	23609		2.74	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	37123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
886	13625		2.24	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2273	14999	27737	7.47	7.8E-01	AW960567.1	EST_HUMAN	EST171637 MAGF resequences, MAGF Homo sapiens cDNA
4653	17387	30020	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5978	18760	31724	2.28	7.8E-01	AF115656.1	NT	Sphenodon punctatus alpha encase mRNA, partial cds

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31871	0.88	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6371	19140	32136	0.83	7.8E-01	AL445086.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8389	21082	34216	1.02	7.8E-01	BF108927.1	EST_HUMAN	7154405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3625176 3'
9133	21821	34987	1.3	7.8E-01	Y10159.1	NT	D. discoideum recGAP gene
9231	21910	35083	0.51	7.8E-01	4826873	NT	Homo sapiens nucleoprotein 214kD (CAIN) (NUP214), mRNA
10024	22672		0.97	7.8E-01	Q26452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12271	25275		2.5	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-aminio-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
139	12954	25596	7.61	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
708	13483		2.26	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (I-Aalpha) and major histocompatibility protein class II beta chain (I-Ebeta) genes, complete cds; butyrophilin-like (NGR), butyrophilin-4>
2717	15424	28163	2.21	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3351	16111		0.84	7.7E-01	8393408	NT	Homo sapiens, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3586	16340	28985	3.88	7.7E-01	AF118085.1	NT	Homo sapiens P101975 mRNA, complete cds
4365	17103	29738	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4365	17103	29739	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31165	1.45	7.7E-01	P16653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5473	18272	31166	1.45	7.7E-01	P16653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5896	18653	31604	0.95	7.7E-01	R08600.1	EST_HUMAN	Y124502.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9744	22395	35900	0.51	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12161	24844		4.55	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6008	18789	31751	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6008	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6425	10193	32189	0.81	7.6E-01	P37938	SWISSPROT	MATNG-TYPE PROTEIN A-ALPHA Z4
6761	17920	30555	0.94	7.6E-01	A1253398.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6761	17920	30585	0.94	7.6E-01	A1253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6851	19433	32449	0.88	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-tetradin receptor mRNA, complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7964	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8026	20721	33852	1.88	7.6E-01	6857752	NT	Mus musculus activin (Activ-pending), mRNA
8028	20721	33853	1.88	7.6E-01	6857752	NT	Mus musculus activin (Activ-pending), mRNA
8866	21557	34703	0.74	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b6, phenobarbital inducible, type a (Cyp2b6), mRNA
9179	21849	35015	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.88	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11330	24021	37328	2.88	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11711	24308		3.64	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11831	24489		3.73	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
500	13284		1.44	7.6E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
570	13351	25878	1.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3354	18114	28769	0.95	7.6E-01	C14203.1	EST_HUMAN	C14203 ClonTech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-037E11 5'
7421	20088	33186	1.01	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11177	23844	37130	1.5	7.5E-01	AB047819.1	NT	Homo sapiens GCMA/GCM1 gene for chorion-specific transcription factor GCM1, complete cds
12228	24882		4.8	7.6E-01	AF163161.2	NT	Homo sapiens derlin sialophosphoprotein precursor (DSPP) gene, complete cds
12742	25008	30975	1.46	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1108	13866	28522	1.78	7.4E-01	AI598146.1	EST_HUMAN	tn14b00.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2342	15065	27802	0.98	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
4276	17016	28842	4.73	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7743	20439	33662	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7743	20439	33663	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8631	21223	34365	0.83	7.4E-01	BF346266.1	EST_HUMAN	602018468F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4164340 5'
8613	21305		0.78	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
8894	21684	34834	6.95	7.4E-01	BE747603.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9054	21743	34901	1.14	7.4E-01	AA187986.1	EST_HUMAN	zp07h01.s1 Strazigene endoferral cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42882 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10302	22949	36184	0.76	7.4E-01	11424933	NT	Homo sapiens NY:REN-46 antigen (LOC51133), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11695	24260	37582	1.85	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11695	24260	37583	1.85	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11900	24467		3.62	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1ih), mRNA
12008	24542						
2989	15765	28413	1.78	7.4E-01	A1472841.1	EST_HUMAN	h13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4575	17310	29838	0.8	7.3E-01	P08710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (TRL1) (TRL1)
4652	17386	30019	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
5040	17759	30373	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HIT017 mRNA, complete cds
6511	19276	32276	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6511	19276	32277	5.92	7.3E-01	L35772.1	NT	Mus musculus arigen (CD72) gene
6594	25103	32735	5.92	7.3E-01	L35772.1	NT	Mus musculus arigen (CD72) gene
7359	20040	33118	0.87	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7445	20121	33210	0.86	7.3E-01	Z14133.1	NT	D.melanogaster C10 mRNA for clathrin heavy chain
7445	20121	33211	7.84	7.3E-01	M26511.1	NT	V.algindicus sucrase (scrB) gene, complete cds
11407	24056	37361	7.84	7.3E-01	M26511.1	NT	V.algindicus sucrase (scrB) gene, complete cds
11407	24056	37362	3.83	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431798 3'
812	13583		3.89	7.2E-01	L29281.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431798 3'
1950	14685	27368				NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2463	15181	27920	2.32	7.2E-01	X78140.1	NT	N.tubacum Nef-1A13 mRNA
3063	15828	28473	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3445	16201	28851	1.38	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3601	16354	28904					
4040	16786		2.56	7.2E-01	AF066608.1	NT	Giardia intestinalis: variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
4718	17450	30083	1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
5075	17764	30410	0.7	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
7112	19800	32864	2.65	7.2E-01	D90314.1	NT	L.messemeriae gene for sucrose phosphorylase (EC 2.4.1.7)
8353	21046	34183				SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
8882	21553		0.74	7.2E-01	P30066	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
10239	22867	36100	0.88	7.2E-01	U69633.1	NT	Oryzias latipes RING-finger binding protein mRNA, partial cds
10639	23330	36568	1.11	7.2E-01	AF236061.1	NT	Oryzias latipes RING-finger binding protein mRNA, partial cds
11104	23774	37049	0.46	7.2E-01	AF743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
			2.33	7.2E-01	AF743773.1	EST_HUMAN	60218381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
			4.02	7.2E-01	BF670061.1	EST_HUMAN	Rattus norvegicus cytochrome mRNA, complete cds
					U82623.1	NT	Dbs-Dbl guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12422	24798		2.9	7.2E-01	AP000003.1	NT	Aeropyrum pernix genomic DNA, section 6/7
676	13451	28094	12.73	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3059	15825	28470	11.78	7.1E-01	AJ270777.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 15-16
4184	16925	29555	3.18	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
4184	16925	29556	3.18	7.1E-01	7305360	NT	Mus musculus obogelin (Obog), mRNA
5858	18045	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
5858	18045	31586	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6850	19550	32580	7.68	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8091	20785	33916	0.56	7.1E-01	H54244.1	EST_HUMAN	yc89d09.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:202961 3'
8635	21327	34469	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301298-011-409 BT0567 Homo sapiens cDNA
8635	21327	34470	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301298-011-409 BT0567 Homo sapiens cDNA
9755	22406	35613	1.43	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22956	36172	1.22	7.1E-01	M12861.1	NT	Human T-cell receptor gamma-chain J2 gene
12211	25203		2.21	7.1E-01	AA421492.1	EST_HUMAN	z106111.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1207	13958	26624	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1207	13958	26625	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2450	15169	27907	1.13	7.0E-01	N62412.1	EST_HUMAN	yz73407.s1 Soares multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2450	15169	27908	1.13	7.0E-01	N62412.1	EST_HUMAN	yz73407.s1 Soares multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
4696	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5862	18849		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8276	20970		11.76	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9216	21895	35064	0.57	7.0E-01	U53898.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlB, mtlF, and mtlD genes, complete cds
9216	21895	35065	0.57	7.0E-01	U53898.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlB, mtlF, and mtlD genes, complete cds
10526	23172	36400	0.49	7.0E-01	U34892.1	NT	Danio rerio complement factor B mRNA, complete cds
11064	23734	37006	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11064	23734	37007	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
949	13715	26380	11.02	8.9E-01	U69874.1	NT	Candida albicans equine sporidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
949	13715	26381	11.02	6.9E-01	U98074.1	NT	Candida albicans: squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.9E-01	AA593530.1	EST_HUMAN	hm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085178 3'
3213	15978	28627	1.97	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5694	18488	31409	0.91	6.9E-01	AB035662.1	NT	Brachyotoma belcheri BBN43 mRNA for notochord actin, complete cds
5900	18685	31633	0.82	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6277	19050	32027	1.36	6.9E-01	BE206188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632328 5'
7687	20360	33474	0.65	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7879	20574	33701	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9069	21768		0.79	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9564	22247	35431	0.69	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9564	22247	35432	0.69	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23888	37172	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11223	23888	37173	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11878	25197		3.01	6.9E-01	Q99068	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
937	13704	26366	1.05	6.9E-01	AF017784.1	NT	Gardia intestinalis carbamate kinase gene, complete cds
2880	15389		0.99	6.9E-01	D80917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14356	27045	1.49	6.9E-01	AA854475.1	EST_HUMAN	q175a06.s1 Soares parathyroid tumor NIH/PA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X58411.maf1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4533	17268	28901	1.45	6.9E-01	J00762.1	NT	Rat(hooded) prolactin gene: exon III and flanks
9538	22191	35375	1.45	6.9E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23699	36982	1.92	6.9E-01	AJ276675.1	NT	Stagonospora avirase bgl1 gene for beta-glucosidase, exons 1-4
11027	23699	36983	1.92	6.9E-01	AJ276675.1	NT	Stagonospora avirase bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11058	23728	37001	2.4	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG20, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37527	1.36	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG20, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1.36	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG20, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
291	13097	25739	44.11	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27606	1.73	6.7E-01	AA451884.1	EST_HUMAN	z012g12.s1 Sources: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2163	15587	27628	2.51	6.7E-01	AF188073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2094	15760	28408	3.41	6.7E-01	6676580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29786	0.79	6.7E-01	X74421.1	NT	S. tuberosus mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30832	0.94	6.7E-01	J04836.1	NT	M. berkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30833	0.94	6.7E-01	J04836.1	NT	M. berkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	19005	31981	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6231	19005	31982	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7215	19000		4.34	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240	19925	33000	0.92	6.7E-01	AE001496.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.68	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23553	36800	2.07	6.7E-01	BF364649.1	EST_HUMAN	GM3-HT0769-010000-197-c03 HT0769 Homo sapiens cDNA
11436	23203	36435	3.59	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11659	24255	37578	1.66	6.7E-01	AA342521.1	EST_HUMAN	EST48085 Fetal spleen Homo sapiens cDNA 3' end
2606	15222	27984	1.29	6.6E-01	AF076240.1	NT	Homo sapiens SIRT1 protein (SIRT1) mRNA, partial cds
2704	16411	28148	1.44	6.6E-01	AF196339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	16403	28043	4.57	6.6E-01	Y07699.1	NT	C. albicans random DNA marker, 282bp
4089	16832		0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRat gene, and sodium phosphate transporter (NPT3) gene, complete cds
5125	17843	30461	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
6240	19014	31998	4.20	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7686	20293	33359	3.76	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLC1D04 3'
8464	21166	34299	0.52	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9664	22217		2	6.6E-01	AL169278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12470	24636	31033	1.48	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
610	13386	26019	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
610	13388	28020	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3428	18183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	18990	29815	4.23	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4277	17016	29843	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5003	17728	30329	2.6	6.5E-01	U28021.1	NT	Phaeosinus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25067	30843	1.77	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TTF4)
5627	18424	31337	0.62	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS210049
6625	19387	32400	1.5	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
7566	20238	33340	0.84	6.5E-01	AJ798882.1	EST_HUMAN	nc46a02.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321842 3'
9737	22388		0.8	6.5E-01	T78904.1	EST_HUMAN	yc21b04.s1 Scars fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108847 3'
10233	22881	36094	1.08	6.5E-01	AF119678.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10529	23228	36400	2.68	6.5E-01	H87583.1	EST_HUMAN	yw1706.r1 Scars placenta_8to9weeks_2NbpP8b0W Homo sapiens cDNA clone IMAGE:252515 5'
10595	23280	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	nc15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10690	23381		3.93	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLAC1E1 Homo sapiens cDNA clone IMAGE:1007810 5'
11599	24198	37518	2.42	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12267	24710		2.07	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12504	25146		1.81	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097C
245	13054	25694	8.05	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dyshen light chain mRNA, complete cds
2503	15307	28043	1.16	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tryptophan halogenase (pmA) gene, complete cds
3449	16205	28855	2.16	6.4E-01	U48854.2	NT	Mus musculus dyaloglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3842	16593	28230	1.06	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
8510	21202	34347	1.82	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
9889	22637	35848	8.6	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10004	22652	35864	1.22	6.4E-01	BF070405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12382	24777		5.99	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGC08 5'
425	13211	25658	4.58	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHIRP-III)
522	13306	25638	2.25	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2159	14889	27623	2.02	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2583	15287	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15297	28036	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds



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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6073	18765	31716	0.94	6.3E-01	BE083906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19289	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6504	19289	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8419	21112		3.44	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3969361 5'
8784	21478	34824	0.95	6.3E-01	S82927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9320	21987	35159	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627521	NT	Varicella virus, complete genome
9838	22489		0.67	6.3E-01	AE002326.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10326	22073	36183	1.47	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36284	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	AW795396.1	EST_HUMAN	PMO-UM0018-1:0500-003-q12 UM0018 Homo sapiens cDNA
10993	23867	36824	2.21	6.3E-01	AA877715.1	EST_HUMAN	m00406.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916 HLARK ;
11306	23967	37268	9.25	6.3E-01	A1904180.1	EST_HUMAN	CM-BT043-080739-046 BT043 Homo sapiens cDNA
11402	24051	37355	1.68	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11581	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11986	25355	30607	4.37	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 8g (K12-8g), mRNA
12078	24587		1.45	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12263	25272		2.93	6.3E-01	X83628.1	NT	C.limicola pecD gene
5780	18571	31489	2.31	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL_142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7364	20073		3.44	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (CaSR-r4) mRNA, partial cds
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	ys01608.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213542 3'
8755	21447	34585	0.52	6.2E-01	AF034411.1	NT	Lycopodium obscurum cytochrome Cu,Zn superoxide dismutase (Sod) gene, partial cds, and dehydroquinase
9349	20420	33540	1.55	6.2E-01	BE962687.1	EST_HUMAN	dehydroase/alkyltransferase/NADP oxidoreductase gene, complete cds
9410	22072		2.55	6.2E-01	M24461.1	NT	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680010 5'
9878	22626	35834	6.2	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35982	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36308	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.38	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spac), mRNA
5449	18248	31137	1.15	6.1E-01	M58040.1	NT	Caenorhabditis elegans N2 CehlydD (hly-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6920	19556	32702	0.84	6.1E-01	AW105853.1	EST_HUMAN	xd50h03.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7005	19897	32751	0.72	6.1E-01	Q63708	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8132	20826	33982	3.27	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8604	21388	34528	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21388	34529	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9315	21982	35153	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21982	35154	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22393	35597	0.93	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
9946	22594	35797	1.06	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11738	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30899	2.28	6.1E-01	AB041350.1	NT	Mus musculus Cdk4b5 mRNA for type IV collagen alpha 5 chain, complete cds
12094	24977		1.57	6.1E-01	X96287.1	NT	M.mazal orfA, orf3, and orfC of archaeal ABC-transporter system
482	13267	25903	1.24	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
548	13331		3.09	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20), mRNA
1341	14089	26765	1.91	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH63-53b attachment protein (G) gene, complete cds
3785	16547	29180	0.92	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF068895.1	NT	Homo sapiens Nctf33 (NOTCH3) gene, exons 26, 27, and 28
5199	18007	30828	2	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18156	30839	2.86	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B11-seb-e-110-UJ.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6445	19213	32210	2.78	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6563	19328	32335	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7254	19938	33013	6.99	6.0E-01	AJ277661.1	NT	(CDW136) (CD136 ANTIGEN)
8023	20718	33850	4.39	6.0E-01	P02835	SWISSPROT	Homo sapiens perlecan LMO1 gene for LIM domain only 1 protein, exon 1
8023	20718	33851	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22374	35574	1.61	6.0E-01	AB008183.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
10173	22821		1.46	6.0E-01	Q01497	SWISSPROT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10990	23664	36921	1.49	6.0E-01	AJ131892.1	NT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10990	23664	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11540	24140	37449	3.77	6.0E-01	AI420623.1	EST_HUMAN	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
12354	24758	31080	2.25	6.0E-01	11421683	NT	HO0807.X1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
12455	24824		2.6	6.0E-01	AA706087.1	EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12639	25208	30815	3.04	6.0E-01	9053303	NT	209605.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12664	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
980	13745	28407	1.36	5.9E-01	U32701.1	NT	RC1-H170375-030-016-c03 HT0376 Homo sapiens cDNA
3264	16026	28675	2.29	5.9E-01	AL163267.2	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3264	16026	28676	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21O067
4186	16937		4.21	5.9E-01	AF162766.1	NT	Homo sapiens chromosome 21 segment HS21O067
6373	19142	32139	1.55	5.9E-01	AF065440.2	NT	Rattus norvegicus casein 2 mRNA, partial cds
7163	19653	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7293	19078		0.61	5.9E-01	X08801.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7899	20563	33725	0.46	5.9E-01	D90911.1	NT	G. gallus gene for skeletal alpha-actinin, exon EF2
8536	21228	34370	0.48	5.9E-01	D12822.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576563-1719843
9443	22120	35239	0.82	5.9E-01	AF063204.2	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9813	22464		0.74	5.9E-01	P08463	SWISSPROT	Chlamydia trachomatis strain K/UW-31/Cx major outer membrane protein (omp1) gene, complete cds
10088	22738	35951	1.15	5.9E-01	P55284	SWISSPROT	E6 PROTEIN
10599	23264	36502	2.5	5.9E-01	Q9X0I3	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10576	23271	36507	1.72	5.9E-01	AF197944.1	NT	THYMIDYLATE KINASE (DTMP KINASE)
10881	23561	36808	2.91	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11149	23616	37099	1.95	5.9E-01	AF064926.1	EST_HUMAN	PM1-DT0041-190j00-002-h03 DT0041 Homo sapiens cDNA
11458	24062	37368	1.56	5.9E-01	P47135	SWISSPROT	Mus spreus strain SPRE1/EI CD48 antigen (Cd48) gene, partial cds
11458	24062		1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN

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## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11458	24082	37389	1.56	5.9E-01	P47135	JSN1 PROTEIN	
12021	24548	31109	2	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12252	24698		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for oridine-5'-phosphate decarboxylase, complete cds
12465	24832		5.72	5.9E-01	P34826	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1902	14639	27348	1.36	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2569	15283	28021	1.01	5.8E-01	7306230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	28838	4.37	5.8E-01	AB008077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
5290	18095		0.82	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5444	18243	31131	0.62	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18669	31835	1.09	5.8E-01	D78659.1	EST_HUMAN	HUM500E088 Human placenta polyA+ (Tfujitara) Homo sapiens cDNA clone GEN-500E08 5'
6220	18894	31970	0.68	5.8E-01	D50601.1	NT	Shigella sonnei LNA for 28 ORFs, complete cds
6715	19630		2.48	5.8E-01	S85091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.61	5.8E-01	H41571.1	EST_HUMAN	Yn9103.s1 Soere adult brain N2b5-IB55Y Homo sapiens cDNA clone IMAGE:175767 3' similar to
7985	20680	33805	0.64	5.8E-01	AI280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
7985	20680	33806	0.84	5.8E-01	AI280051.1	EST_HUMAN	gb:85410.x1 Soere NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8789	21481	34628	8.97	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8871	21592	34707	0.99	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
8872	21593	34708	0.51	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F48F22 IN CHROMOSOME X
9496	22149		0.81	5.8E-01	BF031606.1	EST_HUMAN	601567774F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827298 5'
10911	23591	38837	7.56	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10982	23638		3.97	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
11089	23769		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
1480	14227	28812	1.12	5.7E-01	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
1480	14227	28813	1.12	5.7E-01	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.69	5.7E-01	6755253	NT	Mus musculus plasminogen variant translocation 1 (Pvt1), mRNA
3217	15880	28631	1.62	5.7E-01	Q9W7J2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3495	16251		2.82	5.7E-01	AB033503.1	NT	Populus euphratica pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
8282	18036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	601454932F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3858590 5'
8611	18374	32388	0.81	5.7E-01	AA194201.1	EST_HUMAN	z38006.t1 Soere NHIMPu S1 Homo sapiens cDNA clone IMAGE:686874 5'
8763	17932	30588	1.33	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7664	20328	33438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5OR) (P5C REDUCTASE)
7870	20565		0.5	5.7E-01	AJ251835.1	NT	Mus musculus Kinq1, Lrp5, Mash2, Tesc1, Tesc4 and Tesc8 genes, alternative transcripts
8279	20973		0.47	6.7E-01	AI086081.1	EST_HUMAN	HA0895 Human fetal liver cDNA library/Homo sapiens cDNA
9699	22350	35544	1.19	6.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9699	22350	35545	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	36361	0.72	6.7E-01	BF640362.1	EST_HUMAN	60208712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4006610 5'
11983	24524		1.52	6.7E-01	BE719051.1	EST_HUMAN	MR3-HT0736-181700-003-002 HT0736 Homo sapiens cDNA
12658	24958		3.01	5.7E-01	BE569722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3357	16117	28772	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3357	16117	28773	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3863	16613	29252	0.97	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	16956	29578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21394	34541	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK/Homo sapiens cDNA clone GKCF5F05 5'
8702	21394	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK/Homo sapiens cDNA clone GKCF5F05 5'
9275	22029	35199	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MLG3A gene for intestinal mucin, partial cds
11884	24467		2.57	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11897	24535	37272	1.63	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCL_GGAP_P18 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12352	18613	29252	1.69	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12379	24776		2.7	5.6E-01	P50905	SWISSPROT	HIGH AFFINITY FOTASSIUM TRANSPORTER
12773	25027		4.28	5.6E-01	BF573828.1	EST_HUMAN	602132023F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	26806	0.85	5.6E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2705	15412	28149	0.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28150	0.93	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2919	16985	28330	1	5.5E-01	5902085	NT	Homo sapiens superfamily viralidic activity 2 (S. carvisles homolog)-like (SKIV2L), mRNA
3002	15828		1.55	5.5E-01	H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5B1B56Y Homo sapiens cDNA clone IMAGE:178208 3'
3228	15901	28844	4.22	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3678	16431	29073	1.7	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.79	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BclA-DIB1 gene, partial cds
7187	18873		0.66	5.5E-01	AB015598.1	NT	Cerastium auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	AI791766.1	EST_HUMAN	or82001.y5 NCL_GGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9687	22319		0.7	5.5E-01	U88415.1	NT	Crimson-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	22924	36136	0.96	5.5E-01	T06047.1	EST_HUMAN	EST02935 Fetal brain, Stratagene (cat#636206) Homo sapiens cDNA clone HFBCQ35
11087	23757	37033	1.05	5.5E-01	BF129407.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12955	25597	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
140	12955	25598	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
571	13352	25980	1.16	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
571	13352	25981	1.16	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1248	13907	26864	3.41	5.4E-01	AW886087.1	EST_HUMAN	QV4-NN0040-071400-100-c04 NN0040 Homo sapiens cDNA
2099	14830		3.43	5.4E-01	AE002247.2	NT	<i>Chlamydomonas reinhardtii</i> AR39, section 74 of 94 of the complete genome
2252	14980	27719	1.91	5.4E-01	AJ276882.1	NT	<i>Drosophila melanogaster</i> mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5066	17785	30402	0.92	5.4E-01	M74439.1	NT	<i>Rattus rattus</i> UDF glucuronosyltransferase gene, complete cds
5571	18398	31278	0.74	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6098	18876	31845	0.83	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
6028	19684	32710	0.87	5.4E-01	BE986692.2	EST_HUMAN	601860276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806080 3'
7235	19920	32983	0.81	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7235	19920	32984	0.81	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7237	19922	32987	1.48	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
9890	22540		2.09	5.4E-01	BF572636.1	EST_HUMAN	[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
11015	23687	36948	2.87	5.4E-01	P36958	SWISSPROT	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243660 5'
11621	24218	37541	3.08	5.4E-01	Q60875	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11621	24218	37542	3.08	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944	24499		3.5	5.4E-01	A1958398.1	EST_HUMAN	W37G04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13462 LAMIN A (HUMAN);
503	13287	25621	1.54	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes. >
2136	14866	27598	1.01	5.3E-01	AF113919.1	NT	<i>Brassica oleracea</i> var. capitata phospholipase D2 (PLD2) gene, complete cds
2136	14866	27697	1.01	5.3E-01	AF113919.1	NT	<i>Brassica oleracea</i> var. capitata phospholipase D2 (PLD2) gene, complete cds
2786	15491	28230	6.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	15491	28231	6.83	5.3E-01	45069328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSCCL) gene, complete cds
4187	16928		1.58	5.3E-01	U39687.1	NT	Myoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30880	1.96	5.3E-01	AB20921.1	EST_HUMAN	z442h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30881	1.96	5.3E-01	AB20921.1	EST_HUMAN	z442h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5466	18265	31156	0.84	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares NIHMFU S1 Homo sapiens cDNA clone IMAGE:666112 5'
5466	18265	31157	0.84	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares NIHMFU S1 Homo sapiens cDNA clone IMAGE:666112 5'
5559	18356	31206	1.82	5.3E-01	BE645620.1	EST_HUMAN	7a73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5559	18356	31207	1.82	5.3E-01	BE645620.1	EST_HUMAN	7a73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
8802	21494		1.8	5.3E-01	L01960.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8854	21545	34062	0.81	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
8854	21545	34063	0.81	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
10111	22756	35971	0.82	5.3E-01	AP954210.1	EST_HUMAN	wx94b02.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR;
11550	24149	37490	7.3	5.3E-01	BE586291.1	EST_HUMAN	601339887F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11780	24379	37709	1.72	5.3E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
11877	25206		4.03	5.3E-01	AA916053.1	EST_HUMAN	cg30a05.s1 NCL_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
797	13569	26229	18.35	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1141	13898	28557	8.28	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15)
1189	13923	26385	1.77	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1879	14616		2.35	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2142	14872	27605	2.55	5.2E-01	AB018263.2	NT	Homo sapiens chromosome 21 segment HS21C085
3117	15882	28521	1.23	5.2E-01	U05942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3231	15904		1	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii lsd gene for leucine dehydrogenase, complete cds
3400	16158		1.58	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3437	16193	28843	2.27	5.2E-01	AA984165.1	EST_HUMAN	em77g05.s1 Stratagene ech200 brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16376		0.76	5.2E-01	AF020268.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4588	17303	29630	0.82	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acb), mRNA
4953	17679		1.02	5.2E-01	7106444	NT	Mus musculus vasitollid receptor-like protein 1 (Vt1), mRNA
5567	18364	31272	0.87	5.2E-01	AA284261.1	EST_HUMAN	zfp44d08.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9630	25126	35474	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for Histone H2A, H4 and a histone H3 gene
9630	25126	35475	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for Histone H2A, H4 and a histone H3 gene
9632	22483	35685	0.48	5.2E-01	AA194518.1	EST_HUMAN	zfp5b09.l1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:628783 5'
9926	22574	35772	1.35	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12744	25010		7	5.2E-01	P18510	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
603	13381	26013	1.84	5.1E-01	M58509.1	NT	Human adrenocortical reductase gene, exons 3 to 12
633	13412	26047	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
633	13412	26048	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1848	14394		1.09	5.1E-01	X87885.1	NT	R.norvegicus mtDNA for mammalian fusca protein
2017	14762		1.29	5.1E-01	BF683096.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4057	16802	28433	3.86	5.1E-01	A858495.1	EST_HUMAN	w39b12.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2427263 3'
4164	16804	29633	2.81	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5103	17821	30438	1.01	5.1E-01	U72663.1	NT	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6128	18606	31674	0.67	5.1E-01	BE541068.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6183	18680		0.93	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAF07 5'
6818	19479	32602	1.69	5.1E-01	R80873.1	EST_HUMAN	y84a02.s1 Soares placenta Nb2LpP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34304	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-163400-172-001 ST0023 Homo sapiens cDNA
8470	21162	34305	0.63	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-163400-172-001 ST0023 Homo sapiens cDNA
9583	22238	35420	4.33	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9587	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	85B1 Human retina cDNA Tap509L cleaved sublibrary Homo sapiens cDNA not directional
10090	22708	35926	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	60155863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12326	24745		3.55	5.1E-01	BF439982.1	EST_HUMAN	ncsf1f10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2130	14861	27590	1.24	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2130	14861	27591	1.24	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27801	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2140	14870	27802	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3811	18563	29198	1.13	5.0E-01	L38483.1	NT	Rattus norvegicus legged protein mRNA, complete cds
3864	18604	29241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	19312		0.95	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271839 5'
7582	20232	33334	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7662	20232	33335	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8428	21121		1.92	5.0E-01	M82304.1	NT	Xenopus laevis anodini muscle beta-tropomyosin mRNA, complete cds
8589	21261	34399	0.71	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC 79 Homo sapiens cDNA clone IMAGE:4043485 3'
9368	20429	33647	2.74	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4136832 5'
9525	22178	36382	1.36	5.0E-01	P36573	SWISSPROT	GLYCAGEN DEBRANCHING ENZYME (GLYCAGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	36383	1.36	5.0E-01	P36573	SWISSPROT	GLYCAGEN DEBRANCHING ENZYME (GLYCAGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10290	22938		1.12	5.0E-01	BE889218.1	EST_HUMAN	601445024F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849439 5'
12028	24554		4	5.0E-01	AF029215.1	NT	Mus musculus MFG OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24989		1.86	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
12726	24997		4.39	5.0E-01	O13861	SWISSPROT	NUCLEAR ENVELOPE PROTEIN OUT11
772	13544	29205	2.43	4.9E-01	BF071482.1	EST_HUMAN	602076049F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243860 5'
1856	14402	27090	1.64	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1899	14638	27345	1.15	4.9E-01	U40869.1	NT	Canis porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
5321	18124	30783	0.89	4.9E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31686	3.05	4.9E-01	AF020831.1	NT	Homo sapiens disc glycocalyx kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020831.1	NT	Homo sapiens disc glycocalyx kinase 3 (DAGK3) gene, exon 10
7352	20033	33111	1.91	4.9E-01	AB040081.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10806	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7606	20271	33379	0.84	4.9E-01	Q10806	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8888	21579		1.45	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102503 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9086	21775	34639	0.99	4.9E-01	AW339805.1	EST_HUMAN	h80-c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907268 3' similar to TRC065714
9198	25431		1.98	4.9E-01	10946863	NT	O95714 HERC2.
10216	22884	36076	0.84	4.9E-01	AF063980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10419	23065	36296	0.77	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adoy1) cDNA, partial cds
11925	24488		1.72	4.9E-01	AF176912.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
12709	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
							nc22a1.1.s1 NCL_CGAP_Cof10 Homo sapiens cDNA clone IMAGE:1144862 3'
4288	17037		0.77	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5420	18219	30930	10.78	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6578	19342	32356	0.79	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6889	19352		3.78	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCL_CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217513
7216	19901		1.99	4.8E-01	5031650	NT	Homo sapiens replication 8 (D8S2288E) mRNA
7865	20235	33339	0.78	4.8E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
7861	20325	33434	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7861	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33621	1.2	4.8E-01	A1820744.1	EST_HUMAN	M77f10.y5 Soares breast 2NtHBat Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element;
9144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
10829	23322		1.88	4.8E-01	X83502.1	NT	S. cerevisiae ORF s from chromosome X
12217	25185		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
12795	25219		1.86	4.8E-01	AJ132384.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6422	19190	32186	8.41	4.7E-01	BF217173.1	EST_HUMAN	601863880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
6941	19423	32438	0.94	4.7E-01	AI204374.1	EST_HUMAN	q72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7784	20460	33694	0.83	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
7784	20460	33695	0.83	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8874	21064	34816	0.52	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10751	23436		6.11	4.7E-01	AF102673.1	NT	Influenza A virus isolate h51807 hemagglutinin (HA) gene, partial cds
11022	23694	36957	2.2	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL1A2) gene, exons 6 through 16, and partial cds
11252	23914	37206	1.61	4.7E-01	BF528658.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
11349	24039	37342	1.7	4.7E-01	AW889448.1	EST_HUMAN	RC9-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12116	24609		1.82	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12237	24698		1.51	4.7E-01	AW341591.1	EST_HUMAN	h411c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12813	25055		1.63	4.7E-01	AF000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (7/7)
12817	25300		1.38	4.7E-01	0679502	NT	Mus musculus p16casome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3), mRNA
3726	18479	29116	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3726	18479	29117	1.57	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18136	30785	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5333	18136	30786	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5385	18185	30875	3.11	4.6E-01	Q80649	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5385	18185	30876	3.11	4.6E-01	Q80643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5459	18258	31148	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5472	18271	31163	2.17	4.6E-01	A1247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to
5472	18271	31164	2.17	4.6E-01	A1247679.1	EST_HUMAN	TR-O16338 O16338 BUTYROPHILIN.;
5480	18279	31175	1.8	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5560	18357		0.96	4.6E-01	AF212124.1	NT	Andis schwartzii cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5845	18440		0.77	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
5809	18598	31526	0.59	4.6E-01	D26215.1	NT	Unidentified acil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6163	18940	31911	1.21	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6669	19586	32620	3.2	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6669	19586	32621	3.2	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	25105	32884	0.57	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
7629	20295	33403	0.91	4.6E-01	AA493577.1	EST_HUMAN	nt04h05.s1 NCL_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element ;
7658	20322		0.59	4.6E-01	Q90069	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI>
8219	20973	34049	10.11	4.6E-01	BF697399.1	EST_HUMAN	602130933F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9201	21870	35035	1.11	4.6E-01	P55202	SWISSPROT	ATRIAL Natriuretic Peptide Receptor B Precursor (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source:	Top Hit Descriptor
9201	21870	35036	1.11	4.0E-01	P59202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9876	22526	35720	1.64	4.0E-01	A191663.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9876	22526	35721	1.64	4.0E-01	A191663.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10912	23592		2.3	4.0E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
10922	23602	36850	10.22	4.0E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10922	23602	36851	10.22	4.0E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	36449	5.32	4.0E-01	AF016369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	36450	5.32	4.0E-01	AF016369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24945		1.77	4.0E-01	D53316.1	EST_HUMAN	HUM105F03B Coriell human fetal brain polyA+ mRNA (#9535) Homo sapiens cDNA clone GEN-105F03 5'
1904	14641	27350	1.43	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1904	14641	27351	1.43	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2873	15640	26284	4.5	4.5E-01	AA877088.1	EST_HUMAN	z55402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3312	18072	28722	4.58	4.5E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3372	16131	28787	1.07	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4007	16753		0.95	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4055	18800	29431	0.88	4.5E-01	A1708908.1	EST_HUMAN	es96e09.x1 Baris acid aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4155	17887		4.25	4.5E-01	AW873485.1	EST_HUMAN	h080g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4890	17617	30236	1.1	4.5E-01	BE903445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5461	18260	31151	1.49	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
6510	19276		1.45	4.5E-01	Q00858	SWISSPROT	COAT PROTEIN
7312	19995	33073	1.27	4.5E-01	M37036.1	NT	Rat nuclear proteins B23.1 and B23.2
7509	20180	38273	2.64	4.5E-01	A185849.1	EST_HUMAN	w32a02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR:Q92923 Q92923
7921	20287	39396	0.85	4.5E-01	P60070	SWISSPROT	SWISINF COMPLEX 170 KDA SUBUNIT.1
8206	20900		0.86	4.5E-01	M32061.1	NT	DNA PRIMASE
8302	20906	34134	3.5	4.5E-01	A1848598.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
				4.5E-01			ts5g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8457	21149	34292	0.83	4.5E-01	Q92726	SWISSPROT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
8980	21372		2.34	4.5E-01	11444786	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8897	21588	34728	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
8840	22491		1.02	4.5E-01	9830810	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFBCY17
10392	23038	36255	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFBCY17
10772	23455	36899	2.15	4.5E-01	AW591271.1	EST_HUMAN	x014f01.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11217	23880		1.52	4.5E-01	AV719382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1];
11895	25384		3.52	4.5E-01	BE871401.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLOED12 5'
12540	24880		1.58	4.5E-01	BF337631.1	EST_HUMAN	601449201F1 NIH_MGC_06 Homo sapiens cDNA clone IMAGE:3852981 5'
12811	24918		3.37	4.5E-01	11422009	NT	602035275F1 NCI_CGAP_Brm04 Homo sapiens cDNA clone IMAGE:4183280 5'
2386	15109	27847	3.39	4.4E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3310	16070	28719	1.29	4.4E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	16070	28720	1.28	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3313	16073	28723	2.92	4.4E-01	BF056726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4209	16950		1.88	4.4E-01	BE378707.1	EST_HUMAN	791402.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
5334	18137	30797	1.2	4.4E-01	P04929	SWISSPROT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608383 5'
5334	18137	30798	1.2	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5602	18397	31309	1.59	4.4E-01	S65019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5619	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5804	19651	31591	1.46	4.4E-01	AI198413.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLOCCS12 5'
5864	19651	31592	1.46	4.4E-01	AI198413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29169
6146	19923	31894	1.78	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN ;
6236	19010		1.42	4.4E-01	AA776132.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29188
7297	19980	33056	1.04	4.4E-01	AE000571.1	NT	UNKNOWN PROTEIN ;
7723	25119		0.6	4.4E-01	AE001188.1	NT	xc27e08.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:Q29168 Q29184
7740	20436		9.71	4.4E-01	Z11079.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
8661	21353	34500	0.84	4.4E-01	AA056427.1	EST_HUMAN	ae85d11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:870965 3' similar to gb:M16038
8649	21738	34898	0.7	4.4E-01	AF112840.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
							Helicobacter pylori 26695 section 49 of 134 of the complete genome
							Treponema pallidum section 4 of 87 of the complete genome
							S.tuberculosis mRNA for induced stolon tip protein (partial)
							z69ae03.s1 Stratiogene colon (#837204) Homo sapiens cDNA clone IMAGE:509838 3'
							HIV-1 isolate 08107v8 from USA, envelope glycoprotein (env) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21771	34934	0.57	4.4E-01	AW612578.1	EST_HUMAN	hh05c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6;
9190	21860	35025	1.24	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
9862	22512	35709	2.19	4.4E-01	AI288650.1	EST_HUMAN	q03909.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9863	22513		1.88	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
9897	22845	35857	4.31	4.4E-01	P35580	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36132	1.33	4.4E-01	S78404.1	NT	beta-HKA-H,K-A TPase beta-subunit [rats, Genomic, 8883 nt, segment 2 of 2]
10273	22921	36133	1.33	4.4E-01	S78404.1	NT	beta-HKA-H,K-A TPase beta-subunit [rats, Genomic, 8883 nt, segment 2 of 2]
12148	24635	31095	3.44	4.4E-01	9677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12679	24903	31000	3.35	4.4E-01	9627742	NT	Autographa californica nucleopolydnavirus, complete genome
12683	24971		1.91	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
12766	25152		1.43	4.4E-01	AW363338.1	EST_HUMAN	RC2-CT0320-281189-012-c07 CT0320 Homo sapiens cDNA
402	13187	25835	2.17	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
402	13187	25836	2.17	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2875	15642		1.64	4.3E-01	AW835289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3056	15822	28466	0.75	4.3E-01	AW969477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4131	16873	29501	1.28	4.3E-01	J00306.1	NT	Human somatostatin I gene and flanks
4374	13187	25835	1.18	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4374	13187	25836	1.18	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4902	17628		1.19	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5280	18085	30742	0.8	4.3E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5280	18085	30743	0.8	4.3E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5798	18599	31515	1.59	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
5817	18906	31534	2.02	4.3E-01	AF178825.1	NT	Salinifil sclerous difactory receptor (SSC186) gene, partial cds
6808	19371	32384	4.78	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica lfrG gene
6889	19806	32646	0.6	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
6767	19811		0.91	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4158298 5'
7466	20168	33280	0.61	4.3E-01	U51002.1	NT	Mus musculus Dlx-2 gene, complete cds
8326	21019		2.72	4.3E-01	U87040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9154	21885	35053	0.96	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9626	22279	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868564 5'
9626	22279	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868564 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	22776	35890	0.84	4.3E-01	AW170559.1	EST_HUMAN	xi63405.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10409	23055	36272	0.5	4.3E-01	H65292.1	EST_HUMAN	TR-000189 000189 MU-ADAPTIN-RELATED PROTEIN 2;
10849	19808	32846	2.45	4.3E-01	AF075629.1	NT	y45005.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'
11106	23833	37113	1.29	4.3E-01	AW983658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11106	23833	37114	1.29	4.3E-01	AW983658.1	EST_HUMAN	RC3-BN0034-281200-013-c12 BN0034 Homo sapiens cDNA
11745	24338	37682	1.84	4.3E-01	A187432.1	EST_HUMAN	RC3-BN0034-281200-013-c12 BN0034 Homo sapiens cDNA
12770	25025		2.18	4.3E-01	AJ003022.1	NT	ts84604.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283351 3'
1337	15566	26761	1.54	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
1841	14676		1.23	4.2E-01	AA701653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3596	16349	28960	4.4	4.2E-01	AE003847.1	NT	nt24409.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1286698 3'
3628	16381	28021	1.41	4.2E-01	A1280338.1	EST_HUMAN	Xylella fastidiosa, section 93 of 229 of the complete genome
3698	17888		0.85	4.2E-01	N81203.1	EST_HUMAN	q194b01.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1876945 3'
3984	16713	28352	0.97	4.2E-01	Q04886	SWISSPROT	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4949	17383	30016	4.88	4.2E-01	AA634093.1	EST_HUMAN	SOX-8 PROTEIN
4731	17463	30100	3.46	4.2E-01	R13487.1	EST_HUMAN	ij60h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:907777 similar to gb:M33800 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5626	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	yf77e01.11 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5693	18487	31408	1.53	4.2E-01	AW854162.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108463 5'
6112	18889	31858	1.01	4.2E-01	AL169247.2	NT	RC3-CT0264-060400-028-g04 CT0264 Homo sapiens cDNA
6852	19552	32582	10.8	4.2E-01	AU158472.1	EST_HUMAN	Homo sapiens chr1 chromosome 21 segment HS21C047
6852	19552	32583	10.8	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLAC12 Homo sapiens cDNA clone PLACE2000470 3'
6891	25101	32694	2.15	4.2E-01	S82504.1	NT	AU158472 PLAC12 Homo sapiens cDNA clone PLACE2000470 3'
6893	19686	32734	7	4.2E-01	AL161547.2	NT	Brcal=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7891	20586	33715	2.21	4.2E-01	AW957448.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7891	20586	33716	2.21	4.2E-01	AW957448.1	EST_HUMAN	EST389413 MAGE3 resequences, MAGE Homo sapiens cDNA
8106	20800	33932	0.61	4.2E-01	4758039	NT	EST389413 MAGE3 resequences, MAGE Homo sapiens cDNA
9870	22520		0.94	4.2E-01	AA705007.1	EST_HUMAN	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10081	22729	35944	0.45	4.2E-01	AF181854.1	NT	z65f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10393	23039	36266	1.78	4.2E-01	AW863666.1	EST_HUMAN	Lessa virus strain 303213 glycoprotein precursor and nucleoprotein genes, complete cds
10972	23848	36901	2.69	4.2E-01	AB023489.1	NT	MF3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
11370	23977	37277	2.11	4.2E-01	BE966485.2	EST_HUMAN	Oryzias latipes OK3C7 mRNA for membrane guanylyl cyclase, complete cds
1072	13830	28488	1.93	4.1E-01	A1905481.1	EST_HUMAN	RC-BT091-210194-142 BT091 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13038	26497	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1081	13839	26498	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2715	15422	26161	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2941	15706	26355	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2941	15706	26356	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16506	26142	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGIE resequences, MAGG Homo sapiens cDNA
3754	16506	26143	0.68	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGIE resequences, MAGG Homo sapiens cDNA
4241	16882	26907	2.93	4.1E-01	AL249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE and isoAF genes
4271	17011		0.82	4.1E-01	AA090257.1	EST_HUMAN	om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4618	17353	26688	1.46	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
4668	19057	26706	2.48	4.1E-01	AA080344.1	EST_HUMAN	g94d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1503943 3'
5999	19684	31632	4.72	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7332	20014	33092	2.76	4.1E-01	U67635.1	NT	Methanococcus jenningsii section 77 of 150 of the complete genome
7935	20630	33757	1.38	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
8688	21678	34827	1.39	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Stipee-pending), mRNA
9465	22075		0.67	4.1E-01	AF160597.1	NT	Voelvo gymnocaudus Vgym500 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
10163	22811		1.05	4.1E-01	AL139076.2	NT	mitochondrial product
10310	22857	36173	0.91	4.1E-01	AV649578.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10404	23050	36267	0.61	4.1E-01	P18584	SWISSPROT	AV649578 GLC Homo sapiens cDNA clone GLCBVD12 3'
10404	23050	36268	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (56 KDA IMMUNOGENIC PROTEIN) (SK59)
10478	23124		1.33	4.1E-01	BF349382.1	EST_HUMAN	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (56 KDA IMMUNOGENIC PROTEIN) (SK59)
10743	23430	36673	60.48	4.1E-01	X98700.1	NT	GM2-HT0137-20X698-010-c08 HT0137 Homo sapiens cDNA
11368	23177	36404	2	4.1E-01	Q90470	SWISSPROT	Zea mays ZmPMS2 gene for 19 kDa zein protein
12475	25390		2.62	4.1E-01	D87675.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1)(HUK1)
1016	13776	26435	0.82	4.0E-01	8404656	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1316	14065	26739	0.95	4.0E-01	AF203478.1	NT	Laqueus rubellus mitochondrion, complete genome
1468	14215		4.05	4.0E-01	6879258	NT	Drosophila melanogaster Delmatian (dmt) mRNA, complete cds
1999	15583	27457	1.16	4.0E-01	Z96933.1	NT	Mus musculus plectel derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1999	15583	27458	1.16	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2156	14886	27619	1.19	4.0E-01	AE001931.1	NT	Ascaris lumbricoides msc2 gene
2156	14886	27620	1.19	4.0E-01	AE001931.1	NT	Deinoceratus radicularis R1 section 68 of 229 of the complete chromosome 1
2808	12952	25595	1.4	4.0E-01	6678490	NT	Deinoceratus radicularis R1 section 68 of 229 of the complete chromosome 1
							Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2968	16734	28383	1.1	4.0E-01	AL163280.2	NT	Homo sapiens c11orf105 21 segment HS21C080
2968	16734	28384	1.1	4.0E-01	AL163280.2	NT	Homo sapiens c11orf105 21 segment HS21C080
3683	19438	29080	1.98	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (y1C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3807	16559	29191	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
3807	16559	29192	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
4767	17499		7.97	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5820	18609	31538	1.23	4.0E-01	AW970610.1	EST_HUMAN	EST382081 MAGIE resequences, MAGK Homo sapiens cDNA
6346	19116	32104	0.94	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7728	20391	33504	0.86	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7829	20524	33649	0.44	4.0E-01	BF092634.1	EST_HUMAN	MF4-TN0110-18000-202-g02 TN0110 Homo sapiens cDNA
7910	20606	33736	1.04	4.0E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
8904	21595	34739	1.17	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030262.1	EST_HUMAN	801558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828062 5'
11721	24315		2.83	4.0E-01	L78080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12162	25222		2.26	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12884	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1356	14104	26780	1.85	3.9E-01	AF208818.1	NT	Gorilla gorilla cart-oxyl-ester lipase (CEL) gene, complete cds
2648	15358	28101	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mifNA for KIAA1183 protein, partial cds
2709	15416	28163	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2709	15416	28164	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3083	15858	28499	4.73	3.9E-01	AJ225898.1	NT	Shortholzbium melioli egl. syB2, oye3 genes and orf3
4059	16804	28435	1.05	3.9E-01	BF592611.1	EST_HUMAN	761d01.x1 NCI_CGAP_Brt16 Homo sapiens cDNA clone IMAGE:3339169 3'
4932	17680	30270	1.74	3.9E-01	BE728667.1	EST_HUMAN	801563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
5843	18631	31586	3.91	3.9E-01	BF208036.1	EST_HUMAN	801862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082065 5'
7854	20549	33674	0.82	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-17089-004-b08 CT0105 Homo sapiens cDNA
8769	21461		0.58	3.9E-01	BF348634.1	EST_HUMAN	802018944F1 NCI_CGAP_Brt67 Homo sapiens cDNA clone IMAGE:4155322 5'
9134	21822	34088	1.26	3.9E-01	AW195888.1	EST_HUMAN	Xr86404.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:084821
9445	22122	35301	1.46	3.9E-01	AI837337.1	EST_HUMAN	094821 KIAA0713 PROTEIN; vfp/6a02.x1 NCI_CGAP_Brt25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22429	36635	3.03	3.9E-01	M19879.1	NT	Human debrin ZT gene, exons 10 and 11, and L1 and Alu repeats
9845	22496		0.58	3.9E-01	11485620	NT	Porphyra purpurea mitochondrion, complete genome
10066	22714	35832	0.77	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
11753	24344	37674	1.47	3.9E-01	AV702823.1	EST_HUMAN	AV702823 ADB Homo sapiens cDNA clone ADBDBE08 5'
11948	25295		3.37	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12066	24581		2.08	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
156	12971		8.33	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1663	14601		1.03	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 18 of 229 of the complete genome
2490	15178	27918	1.29	3.8E-01	U41846.1	NT	Ceanothus laurifolius bruggs acetylcholinesterase (ace-1) gene, complete cds
2576	15290	28027	1.62	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2638	15601	28092	3.96	3.8E-01	6978002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	15769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3043	15809	28456	1.39	3.8E-01	AF043383.1	NT	Pleurococcus americanus aminopeptidase N (ampN) gene, partial cds
3477	16233	28887	7.98	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	AB07219.1	EST_HUMAN	wf38612.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3541	16283		1.22	3.8E-01	AB07219.1	EST_HUMAN	wf38612.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16492	29127	1.15	3.8E-01	BE164080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16847	29287	0.87	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
4043	16788	29416	0.74	3.8E-01	AJ271361.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	19021		0.74	3.8E-01	S46825.1	NT	prion protein [mink, Genomic, 2449 nt]
6528	19294	32286	5.5	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-402 BT0537 Homo sapiens cDNA
6662	19579	32614	4.59	3.8E-01	AJ374801.1	EST_HUMAN	la54f11.x1 Soares total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7416	20093		4.42	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
8196	20890	34028	0.86	3.8E-01	M81395.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8455	21147	34289	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8523	21215	34388	1.02	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8716	21408	34551	1.28	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.95	3.8E-01	TP5413.1	EST_HUMAN	ye43h06.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10695	23388		1.67	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11521	24121		3.18	3.8E-01	BE19219.1	EST_HUMAN	RC0-HT0841-043800-032-b12 HT0841 Homo sapiens cDNA
11693	24288	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	y62h11.1.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11693	24288	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	y62h11.1.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12149	24636		4.76	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12270	25316		2.08	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12384	24779		3.39	3.8E-01	BE829258.1	EST_HUMAN	QV3-ET0063-191700-271-s05 ET0063 Homo sapiens cDNA
12723	24984		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
12771	25291		1.74	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
12788	25040	30966	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27844	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3453	16209	28860	0.84	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	29572	7.39	3.7E-01	A1218707.1	EST_HUMAN	ck39c07.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4286	17025	28651	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-081300-104-502 OT0007 Homo sapiens cDNA
4357	17095	29730	2.55	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5676	18470	31386	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5960	18647	31588	0.9	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6417	19185	32183	0.86	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6436	19204		0.72	3.7E-01	L10353.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7043	19734	32794	3.23	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7685	20349	33463	0.6	3.7E-01	T66802.1	EST_HUMAN	ye50e07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element; contains L1.12 L1 repetitive element
7719	20383	33497	0.56	3.7E-01	AW511328.1	EST_HUMAN	hd45c05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:86324 5'
8227	20921	34059	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8263	20957	34096	0.65	3.7E-01	AA002912.1	EST_HUMAN	ck43b11.s1 NCI C3GAP_La2 Homo sapiens cDNA clone IMAGE:1616701 3'
9101	21789		1.31	3.7E-01	AJ271396.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10069	22717		0.6	3.7E-01	K00891.1	NT	mouse Ig gamma alpha membrane exons region
10110	22758	35970	4.12	3.7E-01	A338411.1	EST_HUMAN	qt46b07.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10764	23448	36690	1.98	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MH-C)
10957	23633	36882	2.81	3.7E-01	AJ267357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ267357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (tDT) (EC 2.7.7.31)
11676	24271	37693	1.43	3.7E-01	D78348.1	EST_HUMAN	HUM230A06B Human aorta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-230A06 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11771	24362		2.87	3.7E-01	6677678	NT	Mus musculus radonblastoma 1 (Rb1), mRNA
11869	24943		2.11	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24568		3.09	3.7E-01	AL243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12488	24947		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075.1 762 (synonym: hmd2) Homo sapiens cDNA clone DKFZp762K075.5
12548	24886	30895	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
254	13062	25701	2.17	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
976	13740		8.22	3.6E-01	U88241.1	NT	Human mlbp gene, partial cds
1291	14040	26713	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soarans infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5
1291	14040	26714	3.83	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soarans infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5
1909	14846	27358	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3
1909	14846	27357	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3
1944	14879	27393	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF068927.1	NT	Rattus norvegicus repeat element associated with the Resgfr1 gene
2267	14983		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.69	3.6E-01	X76725.1	NT	P. irregularis (P3834) gene for actin
2479	15197	27638	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27637	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27950	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-18:099-011-g07 ST0171 Homo sapiens cDNA
2636	15348	28090	1.44	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2900	17884		7.16	3.6E-01	AF100485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3462	16218	28871	2.16	3.6E-01	X76758.1	NT	H. sapiens seroton transporter gene, exons 9 and 10
3462	16218	28872	2.16	3.6E-01	X76758.1	NT	H. sapiens seroton transporter gene, exons 9 and 10
4375	17112	29745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-156:600-014-b12 HT0545 Homo sapiens cDNA
4948	17676	30285	2.38	3.6E-01	AW336393.1	EST_HUMAN	ha02g04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568.3
5298	18103	30762	0.82	3.6E-01	AJ006665.1	NT	Homo sapiens liver gene Intron 5
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	FORMATE HYDROXYGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6388	19155	32154	1.74	3.6E-01	Y10196.1	NT	Homo sapiens PHOX gene
7048	19739		3.2	3.6E-01	R94090.1	EST_HUMAN	y74e08.r1 Soarans fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:275987.5
7163	19899	32943	1.9	3.6E-01	AW027174.1	EST_HUMAN	w72e10.x1 Soarans thymus NHFTH Homo sapiens cDNA clone IMAGE:2513010.3 similar to TR:O15117
8123	20817	33953	0.58	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1]; SCO-SPONDIN

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8900	21591	34731	2.74	3.6E-01	4504950	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504950	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8091	21780	34944	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9299	21966	35139	1.04	3.6E-01	X17550.1	NT	D. melanogaster striped gene, exons 3, 4, 5 & 6
9299	21966	35140	1.04	3.6E-01	X17550.1	NT	D. melanogaster striped gene, exons 3, 4, 5 & 6
9369	21944		0.57	3.6E-01	X62825.1	NT	C. perfringens plc: gene for phospholipase C upstream region containing bent DNA fragment
9763	22414	35621	14.67	3.6E-01	Q63194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893	22543	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-21 1099-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-21 1099-002-b10 CT0222 Homo sapiens cDNA
10894	23544	36791	3.31	3.6E-01	BE902390.1	EST_HUMAN	601679418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11062	23722	36993	4.12	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11421	23188	36419	3.4	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11903	25415		1.83	3.6E-01	Y19210.1	NT	Homo sapiens H-b5 gene for hair keratin, exons 1 to 9
11978	24522		1.4	3.6E-01	D90901.1	NT	Synchromyces sp. PCC8803 complete genome, 3/27, 271600-402289
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 226 of 400 of the complete genome
12135	24624		4	3.6E-01	U68888.1	NT	Mus musculus Errf1 mRNA, complete cds
12493	24850		2.12	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12746	25383		2.23	3.6E-01	AW190229.1	EST_HUMAN	x60e11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.69	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	13482	26132	1.69	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
762	13535	26194	4.25	3.5E-01	BF129796.1	EST_HUMAN	601811080R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615	14362	27053	1.1	3.5E-01	BF310688.1	EST_HUMAN	601804653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1638	14382	27096	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOX-1.4) (MH-3)
2612	15600	28096	1.76	3.5E-01	AA223252.1	EST_HUMAN	z08a09.s1 Striatagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:850872 3'

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	18637		0.86	3.5E-01	AA642138.1	EST_HUMAN	nr60d03.e1 NC1 CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	18672	29598	1.67	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxbb) gene, complete cds
4443	17179	29805	0.94	3.5E-01	BE146885.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4627	17362	29995	1.02	3.5E-01	Y18477.1	NT	Mus musculus Alox12b gene 5' flanking region
4890	17607	30230	4.58	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5251	18057	30685	0.78	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30686	0.78	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5482	18261	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6143	18921		0.98	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-e11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.6	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.11 Scarsis testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1068935
6359	19129	32124	0.68	3.5E-01	U37150.1	NT	G1068935 F10F2.1 ;
6688	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	Bos taurus peptic methionine sulfoxide reductase (msrA) mRNA, complete cds
6856	19438		4.24	3.5E-01	X88505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	S. scrofa mRNA for CD31 protein (PECAM-1)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7970	20685		2.19	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7973	20688	33790	0.71	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8398	21050		0.83	3.5E-01	AF061661.1	NT	RC4-ET0024-261600-014-d07 ET0024 Homo sapiens cDNA
8825	21517	34662	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9636	22288	35481	1.52	3.5E-01	Q07294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9786	22437	35644	5.84	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 6) (BRAIN CALCIUM CHANNEL III) (BIII)
9887	22517	35713	0.96	3.5E-01	BE174794.1	EST_HUMAN	XLaevia gene for albumin including HIP1 enhancer
10635	23327	36584	2.78	3.5E-01	X61084.1	NT	QV2-HT0577-091400-128-d07 HT0577 Homo sapiens cDNA
10846	23625	36875	2.39	3.5E-01	AJ243178.1	NT	C.grieseus rhodopsin gene for opsin protein
10946	23625	36876	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24108	37419	1.34	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11685	24184	37499	1.64	3.5E-01	N75897.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
11618	24216		1.71	3.5E-01	M82885.1	NT	y20H12.1 Soares multiple sclerosis 2NbrHSP Homo sapiens cDNA clone IMAGE:280375 5'
11684	24279	37601	1.51	3.5E-01	L05145.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11776	24367		1.38	3.5E-01	A1064773.1	EST_HUMAN	Human glucokinase (GOK) gene, repeat polymorphism
12063	24576		1.47	3.5E-01	X84565.1	NT	HMA642 Human fetal liver cDNA library Homo sapiens cDNA
12214	24676		2.32	3.5E-01	AE001774.1	NT	S. aureus atpA1 gene for F0(F <sub>1</sub> ) ATP synthase alpha-subunit
							Thermotoga maritima section 88 of 136 of the complete genome

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.6E-01	AE001691.1	NT	Thermotoga maritima section 3 of 138 of the complete genome
12793	25289	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soeris retina N2b-4HR Homo sapiens cDNA clone IMAGE:219597 5'
12793	25289	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	ys84f11.r1 Soeris retina N2b-4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	13468		1.85	3.4E-01	AJ242936.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
955	13720	26386	7.61	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, cds genes, orf222 and partial inaA gene
1303	14052	26725	1.72	3.4E-01	Y00654.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2400	15121	27858	2.62	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3001	15767	28415	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3149	15910	28555	1.08	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28588	6.23	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3338	16098	28749	0.9	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28633	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.69	3.4E-01	BF446010.1	EST_HUMAN	7i94e01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ16
4028	16774		2.38	3.4E-01	AA584196.1	EST_HUMAN	nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4460	17198	29823	0.82	3.4E-01	AF168341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4599	17334	29863	1.54	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-23/200-202-c01 BT0403 Homo sapiens cDNA
4898	17625		3.23	3.4E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCI_CGAP_K43 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5143	17862		0.88	3.4E-01	U79745.1	NT	Homo sapiens serotonin transporter (SERT) gene, promoter region, exons 1B and 2, and partial cds
5599	18394	31304	2.62	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 90
5721	18513		6.09	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Striatogene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
5917	18702		1.89	3.4E-01	L02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5940	18722	31681	0.89	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3838828 3'
6017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	UIH-B11-act-e-12-0-UJ.s1 NCI_CGAP_Su53 Homo sapiens cDNA clone IMAGE:2719582 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6844	19406		1.56	3.4E-01	N96225.1	EST_HUMAN	zb53e12.s1 Soeris_fetal_king_NbHL10W Homo sapiens cDNA clone IMAGE:307342 3'

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	19548	32578	1.02	3.4E-01	AI468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
5959	19441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249395 6'
7806	20601		0.49	3.4E-01	AE000483.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8135	20829	33964	0.6	3.4E-01	Y14930.1	NT	Homo sapiens TCR-RAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF446010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
8386	21078		1.51	3.4E-01	AA337063.1	EST_HUMAN	Q9UJ15 DJ18C8.1;
8461	21153	34296	0.72	3.4E-01	LD4690.1	NT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8751	21443	34590	1.7	3.4E-01		NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9112	21800	34964	4.42	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9112	21800	34965	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9321	21988		0.51	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9346	20417	33536	4.67	3.4E-01	U19492.1	NT	Ephydra fluvialis mRNA for PLC-gammaS, complete cds
9346	20417	33537	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9397	22059	35229	0.5	3.4E-01	AF193857.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9505	22248	35433	1.01	3.4E-01	U68763.1	NT	Dictyostelium discoideum putative GMP receptor CMFR1 mRNA, complete cds
9789	22440	35648	1.86	3.4E-01	AJ225084.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
10376	23022		0.62	3.4E-01	AE004098.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10940	23620		4.72	3.4E-01	AE000681.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10984	23659	36912	2.6	3.4E-01	P06925	SWISSPROT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
11032	23703	36971	2.17	3.4E-01	AF046981.1	NT	PROBABLE E4 PROTEIN
11253	23915	37207	1.61	3.4E-01	M26858.1	NT	Rutillus ercaasi cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11253	23915	37208	1.61	3.4E-01	M26856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11483	24084	37386	1.88	3.4E-01	AB035507.1	NT	Human von Willebrand factor gene, exons 36 and 37
11513	24113	37423	3.65	3.4E-01	AL161515.2	NT	Rattus norvegicus mRNA for e-glycyl-MUC18, complete cds
11786	24376	37706	1.72	3.4E-01	BF061948.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11861	24445	37786	1.58	3.4E-01	U07000.1	NT	7n69d12.x1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:3480846 3'
11881	24455		1.85	3.4E-01	U83604.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12197	24698		11.43	3.4E-01	L26339.1	NT	Human variegation virus putative replicase gene, partial cds
12224	25192		1.01	3.4E-01	BE218652.1	EST_HUMAN	Human autoantigen mRNA, complete cds
							In42n08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
							PTR5 repetitive element;



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25282		2.28	3.4E-01	86838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24781	31036	2.2	3.4E-01	AJ287131.1	NT	Mus musculus SCL, MAP_17, CYP_a, SCL & CYP_b genes
12688	24974		1.82	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
103	12840	25453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
435	13221	25867	0.9	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 45
618	13397	26032	2.01	3.3E-01	7862485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26597	2.85	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	26705	3.76	3.3E-01	BF568890.1	EST_HUMAN	602184018T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1338	14085	26760	1.2	3.3E-01	U43628.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the gamma-inhibitory acid receptor b3 and a5 gene cluster
1601	14347	27036	1.47	3.3E-01	8753685	NT	Mus musculus diacylglycerol 5 (Dgnt5), mRNA
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week (Homo sapiens cDNA 5' end
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2404	15125		4.62	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (rotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2949	15715	28368	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3051	15817	28462	1.48	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3486	16243	28809	1.07	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3789	16541	29176	2.1	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3799	16551	29183	0.97	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT
3932	16882	29323	1.03	3.3E-01	4757739	NT	PROTEINASE (HC-PRO); PROTEIN P3J
3947	16897	29336	1.47	3.3E-01	AL161498.2	NT	Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA
3983	16731	29385	1.79	3.3E-01	AF200446.1	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 10
4334	17073		1.6	3.3E-01	D31662.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4941	17375		1.23	3.3E-01	AF539114.1	EST_HUMAN	Rattus norvegicus DNA for regucalcin, partial cds
4786	17517	30139	1.22	3.3E-01	D64003.1	NT	tp78b12.x1 NCL CGAP_U03 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
5146	17865		0.86	3.3E-01	AW037982.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2888786
5241	18047	30675	2.61	3.3E-01	X89819.1	NT	QV0-DT0047-170200-123-h08 DT0047 Homo sapiens cDNA
5241	18047	30676	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5700	18494	31417	0.74	3.3E-01	BF213873.1	EST_HUMAN	60184800F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
5856	18543	31582	1.9	3.3E-01	BE619660.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
5856	18543	31583	1.9	3.3E-01	BE619660.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
5947	18729	31688	1.18	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6695	19012	32651	0.71	3.3E-01	AB034233.1	NT	Flexibacter libralis gyrB gene for DNA gyrase B subunit, partial cds
6695	19012	32652	0.71	3.3E-01	AB034233.1	NT	Flexibacter libralis gyrB gene for DNA gyrase B subunit, partial cds
6789	19533	32560	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6789	19533	32561	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7882	20346	33458	1.68	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460	21152	34295	18.62	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8659	21351	34497	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351	34498	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9012	21702	34852	0.81	3.3E-01	Q62825	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9278	22032	35203	0.81	3.3E-01	BE828461.1	EST_HUMAN	GM3-ET0041-181500-187-d10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828461.1	EST_HUMAN	GM3-ET0041-181500-187-d10 ET0041 Homo sapiens cDNA
9411	22073	35244	2.62	3.3E-01	N068663.1	EST_HUMAN	za67h01.s1 Soenke_fetal_lung_NibHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9452	22002	35174	2.77	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-281800-011-g04 TN0077 Homo sapiens cDNA
9891	22541		2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10922	23315	36554	3.13	3.3E-01	XG3963.1	NT	D.mauritiana Adh gene
10922	23315	36555	3.13	3.3E-01	XG3963.1	NT	D.mauritiana Adh gene
10951	23628		1.7	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213585 5'
11186	23861	37147	11.61	3.3E-01	BE218351.1	EST_HUMAN	hy51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176878 3'
11317	24008	37313	3.23	3.3E-01	P47863	SWISSPROT	GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11719	24313		3.06	3.3E-01	AA806621.1	EST_HUMAN	cb71g02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11741	12840	25453	1.87	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
11977	24521	37266	1.71	3.3E-01	6598319	NT	Homo sapiens aldohyde oxidase 1 (AOX1), mRNA
12676	24967		3.34	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
701	13476		1.43	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13894	26555	27.53	3.2E-01	AF047013.1	NT	Fusarium rose virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26677	1.36	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1369	14117	26792	5.42	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1767	14509	27210	1.25	3.2E-01	Z30041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27222	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAG3E resequences, MAGD Homo sapiens cDNA
1777	14519	27223	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAG3E resequences, MAGD Homo sapiens cDNA
1835	14574	27286	1.23	3.2E-01	AL111655.1	NT	Boltyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2157	14887	27621	2.52	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2543	15257		2.01	3.2E-01	7710079	NT	Mus musculus P <sub>0</sub> knotted 1 homeobox (P <sub>0</sub> knx1), mRNA
2713	15420	28159	1.08	3.2E-01	AF000568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3594	16347		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4305	17044	29689	0.91	3.2E-01	4759195	NT	Homo sapiens synplekin (SYM) mRNA
4363	17101	29736	1.52	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4484	17200	29828	1.21	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C19G7.04C IN CHROMOSOME 1 PRECURSOR
4688	17422		6.7	3.2E-01	BF663817.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4828	17557	30179	1.17	3.2E-01	Q67081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
4995	17690	30299	0.74	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3688789 5'
5190	17998	30621	3.28	3.2E-01	BE173964.1	EST_HUMAN	CMO-HT0569-061300-269-410 HT0569 Homo sapiens cDNA
5868	18655	31506	1.07	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
6211	18886	31963					Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6501	19266	32266	0.9	3.2E-01	AF018494.1	NT	AV718037 FHITA Homo sapiens cDNA clone FHITAABH01 5'
6634	19396		0.84	3.2E-01	AV718037.1	EST_HUMAN	Human mRNA for KIAA0361 gene, KIAA0361 protein
7755	20451	33575	1.09	3.2E-01	AB002359.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
8072	20766	33895	0.51	3.2E-01	A1277661.1	NT	Rat [SO-atrial natriuretic factor gene, complete cds
8164	20858	33990	1.48	3.2E-01	M80266.1	NT	Rattus norvegicus repeat; map NOS-D12W.ox1
8265	20959		0.45	3.2E-01	A1231001.1	NT	
8265	20959	34098					
8268	20962	34103	14.41	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8361	21054		13.76	3.2E-01	BF311635.1	EST_HUMAN	601867107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126833 5'
			1.38	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8398	21091	34228	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8471	21163	34306	2.65	3.2E-01	AE002015.1	NT	Deltococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8571	21263	34401	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8665	21656	34807	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8976	21696		2.18	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9048	21737	34894	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10099	22747	35862	0.45	3.2E-01	BE326230.1	EST_HUMAN	h6905.1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:3181566 3'
10210	22858		3.41	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10568	23261	36498	3.94	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Strati gene (cat#336206) Homo sapiens cDNA clone HFB0221
12010	25317		3.91	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	25374		1.44	3.2E-01	BE886848.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3609632 5'
12524	24871		4.21	3.2E-01	O63217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12712	25354	30606	1.76	3.2E-01	BE386776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2677	15386	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	ye80h08.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QMPROTEIN (HUMAN);
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	15630		1.29	3.1E-01	AW629036.1	EST_HUMAN	h146h08.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3170	15933		3.35	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KIAARE, exon 6
3887	16637	29276	0.8	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4908	17636	30250	0.73	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5390	18190	30882	9.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1236
5514	18312	31213	0.87	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141W
5524	18322		0.88	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5685	18478	31396	2.11	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R84322.1	EST_HUMAN	ye41f04.1 Soares: fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198367 5'

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6374	19143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-3'10300-011-b04 HN0001 Homo sapiens cDNA
6439	19207	32203	1.01	3.1E-01	A1264458.1	EST_HUMAN	q39d01.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874889 3'
6583	19348	32360	3.91	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6873	25061	30545	2.41	3.1E-01	BE737382.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7579	20248	33354	0.77	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	R45318.1	EST_HUMAN	Yg46f01.s1 Soaris Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
9802	22453	35655	0.54	3.1E-01	6879322	NT	Mus musculus phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma (Pip5K1c), mRNA
9967	22615	35818	1.05	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
9967	22615	35819	1.05	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10028	22677	35893	1.74	3.1E-01	A1244001.1	EST_HUMAN	q61611.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10201	22849		0.63	3.1E-01	T66325.1	EST_HUMAN	y647N08.s1 Stratiogene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:74867 3' similar to similar to gb:M61036_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10741	23428	36672	1.26	3.1E-01	BF216117.1	EST_HUMAN	601863562F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085814 5'
11524	24124	37430	2.56	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	24623		1.48	3.1E-01	AF284308.1	NT	Ancalis opalinus lactate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12165	24647		3.03	3.1E-01	AF304162.1	NT	Sitostacion vitreum 40S ribosomal protein S11 mRNA, partial cds
12304	24729		2.62	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12660	24960		3.46	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$ )
12696	25347		1.35	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA
247	13056	25533	2.01	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc $\epsilon$ ), mRNA
247	13056	25698	14.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudosubosomal region; segment 1/2
1202	13954	26618	2.51	3.0E-01	AW300400.1	EST_HUMAN	x63308.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	14244	26890	6.57	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2132	14862	27592	1.2	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3208	15969		1.18	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyketonate lyase, complete cds
3848	16597	29234	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261188-001-g01 ST0262 Homo sapiens cDNA
4477	17212	29837	1.95	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5267	18073	30702	7.22	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3848734 5'
5349	18152	30833	0.77	3.0E-01	AF228247.1	NT	Canis lupus orthopoxvirus hemagglutinin gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5417	18216	30924	3.94	3.0E-01	BE63575.1	EST_HUMAN	RC3-BT0333-150700-111-e03 BT0333 Homo sapiens cDNA
5417	18216	30925	3.94	3.0E-01	BE63575.1	EST_HUMAN	RC3-BT0333-150700-111-e03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 129/ev Clara cell 10 kd protein (mCG10) gene, complete cds
6732	18566	32598	3.08	3.0E-01	D16313.1	NT	Mouse cytochrome 15 gene, complete cds
6762	17931	30567	0.61	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
6827	19488	32510	0.85	3.0E-01	AF228247.1	NT	Canis familiaris orthoreovirus hemagglutinin gene, complete cds
7021	19713	32770	0.71	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7227	19912	32985	2.77	3.0E-01	10947007	NT	Mus musculus richidin (Mdn-pending), mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PepA (papa) gene, partial cds
7827	20522	33648	1.3	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8271	20965		2.97	3.0E-01	6910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec4e9), mRNA
8374	21067	34207	1.32	3.0E-01	BE560683.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8728	21420	34584	0.51	3.0E-01	AF141678.1	NT	Streptomyces sulfonolactis isopenicillin N synthase (pcbC) gene, partial cds
8770	21462		0.8	3.0E-01	7661685	NT	Homo sapiens DKFZ586M0122 protein (DKFZ586M0122), mRNA
9118	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytochrome-specific DNA methyltransferase (dmnB) gene, complete cds; putative antraxialate phosphotransferase gene, partial cds; and unknown gene
9856	22506		43.84	3.0E-01	BE001129.1	EST_HUMAN	RC2-BN0074-240400-110-h12 BN0074 Homo sapiens cDNA
9868	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 5'
10042	22690	35908	0.49	3.0E-01	AF152598.3	NT	Acetivibacillus actinomyceternomittans Tada (tada), TadaB (tadB), TadaC (tadC), TadaD (tadD), TadaE (tadE), TadaF (tadF), and TadaG (tadG) genes, complete cds
10042	22690	35909	0.49	3.0E-01	AF152598.3	NT	Acetivibacillus actinomyceternomittans Tada (tada), TadaB (tadB), TadaC (tadC), TadaD (tadD), TadaE (tadE), TadaF (tadF), and TadaG (tadG) genes, complete cds
10294	22941	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	xs03410.XT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806035 3'
10296	22943	36157	1.88	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BIP, complete cds
10316	22963	36179	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10316	22963	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
11772	24363	37694	1.95	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:194107 5'
11772	24363	37695	1.85	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:194107 5'
12416	25302		2.52	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12693	25345		5.51	3.0E-01	6877766	NT	Mus musculus rib-see 5-phosphate isomerase A (Rpl), mRNA
2018	14753	27481	1.43	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2245	14973	27710	1.18	2.9E-01	AF222718.1	NT	Chrysothymus synuroideus mitochondrion, complete genome
3246	16908	28658	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171290-001-412 CT0326 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3246	16008	28659	2.73	2.8E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3877	16627	29285	0.72	2.9E-01	A1610836.1	EST_HUMAN	tp21at1.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4052	16797	29427	0.73	2.8E-01	AB016428.1	NT	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4064	16808		0.77	2.9E-01	AW002802.1	EST_HUMAN	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4452	17188	29813	1.1	2.9E-01	AA284468.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
5177	17986		1.66	2.9E-01	R37485.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu
5310	19607	32532	0.79	2.9E-01	AF321001.1	NT	repetitive element;
5677	18471	31387	5.19	2.9E-01	X59086.1	NT	y177e12.s1 Soaris Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5677	18471	31388	5.19	2.9E-01	X59088.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5699	18482	31401	6.4	2.9E-01	6679682	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose 6-phosphotransferase
5965	18747	31708	1.47	2.9E-01	AA418146.1	EST_HUMAN	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose 6-phosphotransferase
6187	18984	31937	1.08	2.9E-01	A1797128.1	EST_HUMAN	system polypeptides P16,18,28,30 and levanase
6233	19007	31984	2.4	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6365	19135	32130	0.58	2.9E-01	R69194.1	EST_HUMAN	zs67b12.r1 Soares NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:707711 5'
6365	19135	32131	0.58	2.9E-01	R69194.1	EST_HUMAN	wet2c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.t1 L1
6621	19383		0.56	2.9E-01	Z50156.1	NT	repetitive element;
6890	17986	30523	1.52	2.9E-01	AF142329.1	NT	Bos taurus myosin I mRNA, complete cds
6898	19688	32737	2.96	2.9E-01	Q04399	SWISSPROT	y339d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
							y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
							D. discoideum gene for 34 kD actin binding protein
							Mus musculus Filh protein (Filh) gene, complete cds; and Lgh protein (Lgh) gene, partial cds
							PUTATIVE MULTICOPPER OXIDASE YDR508C
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bmg1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
7059	19750	32813	2.06	2.9E-01	AF100956.1	NT	
7820	20515	33640	1.67	2.9E-01	BE640422.1	EST_HUMAN	601066830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7820	20515	33641	1.67	2.9E-01	BE640422.1	EST_HUMAN	601066830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33875	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-10
8049	20743	33876	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8052	20758		0.94	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085113 5'
8237	20931		0.49	2.9E-01	AF197456.1	NT	Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	21185	34328	0.84	2.8E-01	AU150910.1	EST_HUMAN	AU150910 NT2-IP2 Homo sapiens cDNA clone NT2RP2003601.3'
8823	21516	34680	1.02	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylesterase receptor-like protein mRNA, complete cds
8931	21822	34765	0.65	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9146	21876	35040	0.78	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9145	21878	35041	0.78	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
10810	23493	36728	1.93	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37059	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37060	1.75	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.59	2.9E-01	AA635373.1	EST_HUMAN	repetitive element
11579	24178	37493	3.55	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11600	24199	37519	1.82	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24199	37520	1.82	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.9E-01	AF082453.1	NT	Homo sapiens TNF- $\alpha$ -inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.86	2.9E-01	Y06937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	Y06937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U67138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
500	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1061	13819	26481	3.69	2.8E-01	AF168050.1	NT	Gultra gultra oocyte maturation factor Mos (c-mos) gene, partial cds
1254	14003	26671	1.82	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE3163688 5'
1254	14003	26672	1.82	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE3163688 5'
1268	14017	26684	1.34	2.8E-01	D96550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF076238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW800020.1	EST_HUMAN	QV1-CT0384-120200-065-505 CT0364 Homo sapiens cDNA
2006	14742	27487	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_11 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i2321
2127	14858	27589	1.41	2.8E-01	AW511195.1	EST_HUMAN	h444803 x1 Soars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2912333 3'
2475	15193	27833	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 394 of 400 of the complete genome
2475	15193	27834	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2649	15284		1.89	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2670	15390	28118	0.97	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2970	15736		1.29	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2971	15737	28386	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3373	16132	28788	1.13	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (47)



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3978	18726	29360	1.59	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4174	18914		1.95	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
4422	17158	29789	0.89	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Cattractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29793	2.31	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30126	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4777	17508	30131	2.67	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	BF528188.1	EST_HUMAN	602042001F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180129 5'
4829	17690	30182	1.91	2.8E-01	AI272680.1	EST_HUMAN	q150c11.x1 Soares_NHT-MP_u_S1 Homo sapiens cDNA clone IMAGE:4180129 5'
5228	25084	30680	24.65	2.8E-01	AA346997.1	EST_HUMAN	repetitive element; contains element LTR5 repetitive element
5519	18317	31218	3.07	2.8E-01	AB016925.1	NT	EST57072 Infant brain Homo sapiens cDNA 5' end
5727	18519		0.95	2.8E-01	AW982563.1	EST_HUMAN	Homo sapiens OATN2 gene, complete cds
5848	18635		0.63	2.8E-01	AA404576.1	EST_HUMAN	CM1-BN0024-151200-118-g12 BN0024 Homo sapiens cDNA
6083	25418		0.85	2.8E-01	M36868.1	NT	z441f01.1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6632	19394	32409	8.34	2.8E-01	BF511216.1	EST_HUMAN	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
7341	20022		1.17	2.8E-01	U059333.1	NT	UI-H-B14-act-f-04-0-ULs1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7382	20062	33140	0.58	2.8E-01	X69080.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7991	20686	33811	1.28	2.8E-01	AI346128.1	EST_HUMAN	L. esculentum ypt2 mRNA for GTP-binding protein
7991	20686	33812	1.28	2.8E-01	AI346128.1	EST_HUMAN	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 80S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U51658.1	NT	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 80S RIBOSOMAL PROTEIN L3 (HUMAN);
8412	21105	34244	0.51	2.8E-01	AA911629.1	EST_HUMAN	Homo sapiens lens-actin 14-alpha demethylase cytochrome P-450 (CYP51) gene, exon 5'
8488	21180	35115	7.34	2.8E-01	BF347847.1	EST_HUMAN	c02h05.x1 NCL CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419093 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8666	21941	35115	0.92	2.8E-01	U17261.1	NT	602022987F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158525 5'
9811	22284		0.88	2.8E-01	L13954.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
9788	22439	35646	0.89	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
						NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35647	0.66	2.8E-01	AF132728.1	NT	Escherichia coli translocated Inlirin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.52	2.8E-01	AF284363.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9960	22608	35813	3.35	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10211	22659		1.47	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome
10251	22699	36109	0.8	2.8E-01	BE959727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839786 3'
10644	23335	36573	2.42	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108950 5'
10644	23335	36574	2.42	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108950 5'
10671	23362	36603	3.83	2.8E-01	BF665070.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076028 5'
10794	23477	36719	1.33	2.8E-01	AF051662.1	NT	Drosophila heterocnema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11247	23909		4.51	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273953 5'
11663	24192	37510	17.66	2.8E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12406	24789		15.41	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12509	24861	31013	4.22	2.8E-01	BE178899.1	EST_HUMAN	PM4-HT0808-031400-001-407 HT0808 Homo sapiens cDNA
12832	24877	31019	1.77	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955898 5'
12865	25306		2.52	2.8E-01	11433628	NT	Homo sapiens C17C42-binding protein kinase beta (DMFK-like) (CDC42BPB), mRNA
12806	25401		1.49	2.8E-01	AW025400.1	EST_HUMAN	Homo sapiens C17C42-binding protein kinase beta (DMFK-like) (CDC42BPB), mRNA
464	13249	26890	3.97	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
589	13377	28007	3.25	2.7E-01	AA450061.1	EST_HUMAN	Z39510.s1 Soares_tet_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:788527 3' similar to contains Alu repetitive element
1238	13987	28654	2.13	2.7E-01	AB004608.1	NT	Ipomoea purpurea transposable element T100 gene for transposase, complete cds
1617	14384		1.58	2.7E-01	X78815.1	NT	G. lamblia SR2 gene
1722	14485	27184	3.5	2.7E-01	W58067.1	EST_HUMAN	zid2h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1769	14511	27212	2.56	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2131	15586		2.25	2.7E-01	AF047576.1	NT	Rattus norvegicus vesicular stomatitis virus type 2, promoter region and exon 1
2367	15089	27826	10.01	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT088P1U (M88), partial
2457	15175	27914	4.07	2.7E-01	AI310858.1	EST_HUMAN	la43c11.x2 NCI_CGAP_Luc25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
2899	15686	28314	1.2	2.7E-01	AF251276.1	NT	Mus musculus sea line protease inhibitor 14 (Spi14) mRNA, complete cds
2983	15749		2.63	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-s05 HT0875 Homo sapiens cDNA
3283	16044	28693	0.68	2.7E-01	8383820	NT	Rattus norvegicus insulin receptor (Insr), mRNA
3992	16740	29374	1.97	2.7E-01	AI928015.1	EST_HUMAN	wo82e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4002	16749	26380	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	16749	26381	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4008	16754	26384	2.12	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4680	17703		2.85	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0288-233200-018-403 CT0288 Homo sapiens cDNA
5011	17733	30339	2.53	2.7E-01	AA100656.1	EST_HUMAN	z80a01.11 Striatogene codon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.53	2.7E-01	AA100656.1	EST_HUMAN	z80a01.11 Striatogene codon (#837204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5185	17993	30509	2.39	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	Astropora myrtillophthalma mitochondrial cytb gene for cytochrome b, partial cds
6249	19023	31995	0.66	2.7E-01	Q00618	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31998	0.66	2.7E-01	Q00618	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6515	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6681	19598	32637	2.23	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32689	0.58	2.7E-01	U15987.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	AF540070.1	EST_HUMAN	h08h08.v1 NCL_X3AP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7258	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0663.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7688	20256	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7688	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7638	20303	33411	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
7638	20303	33412	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
7604	20358	33472	0.71	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7763	20459	33583	0.68	2.7E-01	AA013147.1	EST_HUMAN	z835b1.1.a1 Soera retina N2b-4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7925	20820		0.53	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soas infant brain INIB Homo sapiens cDNA clone IMAGE:23511 3'
8190	20884	34022	0.8	2.7E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.69	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	P37828	SWISSPROT	FIMBRIAE W PROTEIN
9700	22351	35546	0.61	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17 and complete cds
9981	22629	35838	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22666	35882	3.09	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10149	22797	36012	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22797	36013	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10724	23412	36653	3.13	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.6	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.06C
12482	25180		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfite transporter, complete cds
12665	24963		2.83	2.7E-01	AF217491.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 6
12811	25054	30929	1.95	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXR02 5'
457	15542	25883	2.03	2.6E-01	P78411	SWISSPROT	IRQJUIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D19459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	26795	1.65	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1417	14165	26848	1.14	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1899	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1899	14626	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to db:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2086	14818		10.48	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2148	14878	27613	3.7	2.6E-01	M11844.1	NT	B. maritimus rbcL gene
2476	15194		1.62	2.6E-01	Y12966.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	16263		8.87	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960043 5'
3508	16323	28971	8.99	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N0)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4078	16823	29449	0.98	2.6E-01	AW899510.1	EST_HUMAN	EST371590 MA31E resequences, MAGF Homo sapiens cDNA
4134	16876	29506	16.7	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17246	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4901	17336	29885	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds
4957	17401	30035	1.18	2.6E-01	AF142703.1	NT	Opine reductase mature-like protein (maik) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloproteinase disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.8	2.6E-01	H04898.1	EST_HUMAN	Y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5257	18063		1.06	2.6E-01	AB035972.1	NT	Paraneuronal calcium gene for PAP, complete cds
5484	18283		0.88	2.6E-01	AI862398.1	EST_HUMAN	td16a03.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
5888	18481	31400	0.73	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pin-2 protooncogene homolog pin-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g)
5980	25417		2.35	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6108	18885	31854	2.26	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6108	18885	31855	2.26	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6328	19098	32086	0.91	2.6E-01	AL182757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6570	19334	32344	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836158 5'
6570	19334	32345	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836158 5'
6838	19673	32719	0.9	2.6E-01	AI814380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7289	19972	33050	0.82	2.6E-01	BE149661.1	EST_HUMAN	CMO-HT0245-03:199-085-04 HT0245 Homo sapiens cDNA
7329	25110		0.79	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7363	20044		0.89	2.6E-01	AA198149.1	EST_HUMAN	zp92a01.11 Stratigene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672.5'
7639	20304	33413	1.9	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004.3' similar to gb:X12517.1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7687	20351	33485	0.88	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E5.01 IN CHROMOSOME I
7748	20444	33568	1.3	2.6E-01	R02411.1	EST_HUMAN	ye82a07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212.5'
7804	20498	33620	1.15	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0166-181199-003-d12 HT0166 Homo sapiens cDNA
8040	20735	33867	0.84	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8040	20735	33868	0.84	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8232	20926	34064	3.05	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150396.5'
8309	21003	34140	2.13	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8594	21288	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35116	0.98	2.6E-01	X17604.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9639	22291		0.82	2.6E-01	AF057121.1	NT	Loritra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9768	22419	35626	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
9768	22419	35627	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
9830	22578		0.48	2.6E-01	U67581.1	NT	Methanococcus jannaschii section 123 of 150 of the complete genome
10090	22738		0.74	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10406	23052		0.9	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10467	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens NRAMP2 gene for natural resistance-associated macrophage protein 2, complete cds
11400	24006	37310	1.78	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11611	24111		66.41	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11896	24534		1.71	2.6E-01	10180655	NT	Mus musculus Jerky (Jrk), mRNA
12177	25309		3.1	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612.5'
12242	24893	31077	2.81	2.6E-01	AF316898.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
12565	24995		1.56	2.6E-01	D88425.1	NT	CaVia cobyra mRNA for serine/threonine kinase, complete cds
12725	24996		2.19	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
234	13045	25684	2.55	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
235	13045	25084	2.39	2.5E-01	4502206	NT	Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
248	13057		3.32	2.5E-01	M26501.1	NT	Starfish ( <i>P. ochraceus</i> ) cytoplasmic actin gene, complete cds
813	13584	20250	1.35	2.5E-01	U09804.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1038	13798		1.2	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1099	13857	28517	6.42	2.5E-01	T88837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1509	14255	28941	0.9	2.5E-01	AL115624.1	NT	Bovine chereea strain T4 cDNA library under conditions of nitrogen deprivation
1721	14464		4.70	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1876	15581	27323	1.58	2.5E-01	BE698804.1	EST_HUMAN	PM4-CTD400-31:3700-005-d08 CTD400 Homo sapiens cDNA
1876	15581	27324	1.58	2.5E-01	BE698804.1	EST_HUMAN	PM4-CTD400-31:3700-005-d08 CTD400 Homo sapiens cDNA
2407	15128		16	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2500	15217		1.09	2.5E-01	AA231987.1	EST_HUMAN	za11a12.r1 NCL CGAP GC81 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16129		0.84	2.5E-01	BF698193.1	EST_HUMAN	802125525F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4282279 5'
3407	16165		3.04	2.5E-01	AW973471.1	EST_HUMAN	EST385494 IMAGE resequences, MAGM Homo sapiens cDNA
3524	16280	28935	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3828	16570	29211	1.53	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	16579	29212	1.53	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4706	17438	30070	3.89	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapauser associated protein 2 (DAP2) mRNA, complete cds
4732	17464	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ230113.1	NT	Mus musculus aniridin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE698785.1	EST_HUMAN	601437486F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
4987	17710	30315	0.71	2.5E-01	AW873588.1	EST_HUMAN	hs62f11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71PFA_294.D CE22858 ;
5243	18049	30678	13.48	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
5870	18657	31598	0.73	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQ1 gene
5871	18658		0.98	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5829	18295	32298	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens parafibronin-1 gene
5845	19427	32442	0.79	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7252	19638	33011	0.88	2.5E-01	U13892.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19662		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33259	0.83	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 18
7538	20206	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33584	2.47	2.5E-01	BF109040.1	EST_HUMAN	7157403.x1 Soariss NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526389 3'
7764	20460	33574	0.8	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	60145238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8206	20990	34128	0.7	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8534	21228	34368	3.67	2.5E-01	H53236.1	EST_HUMAN	yq84f07.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
8774	21466	34613	0.78	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35295	15.72	2.5E-01	U98651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9416	22094	35296	15.72	2.5E-01	U98651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35253	2.08	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35254	2.08	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9908	22846	35858	1.38	2.5E-01	AW581897.1	EST_HUMAN	RC3-ST0188-130100-016-a07 ST0188 Homo sapiens cDNA
10441	23087	36315	2.13	2.5E-01	AW152246.1	EST_HUMAN	xq40c10.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10444	23090	36319	1.21	2.5E-01	X58491.1	NT	Mouse L1M4 LINE DNA
11013	23685	36945	3.43	2.5E-01	D50614.1	NT	Human mRNA for KIAA0124 gene, partial cds
11047	24244		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
11803	24393	37727	1.29	2.5E-01	U45315.1	NT	Limonosoides signodentis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds
11832	24490	37808	5.12	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
11960	25388		6.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 41
12365	24768		1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genome DNA, 544001-777000 nt. position (3/7)
12412	25233	30821	1.37	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUG mRNA, complete cds
540	13323	25955	1.69	2.4E-01	AA936316.1	EST_HUMAN	on70004.s1 Soariss NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
828	13598	26298	3.34	2.4E-01	BF578124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1281	14031	26700	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1281	14031	26701	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1843	14581		32.88	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1893	14630	27340	1.33	2.4E-01	AF251708.1	NT	Zaocys dharmadasi fructose-1,6-bisphosphatase mRNA, complete cds



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14864	27694	1.1	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2165	14894		1.44	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2258	14985	27725	2.28	2.4E-01	AE000680.1	NT	Aquifex seductus section 12 of 109 of the complete genome
2382	15104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2539	15254	27994	2.46	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A:
2765	15470	28213	2.16	2.4E-01	X71783.1	NT	D.discoideum (A3-K) parA gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3129	15894		2.94	2.4E-01	U72728.1	NT	Bovine adenovirus 3 complete genome
3145	15909	28554	1.48	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3743	16496	29131	0.73	2.4E-01	AE000312.1	NT	H.sapiens AGT gene, PstI fragment of Intron 4
4010	16758		0.74	2.4E-01	D29060.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4883	17610		1.09	2.4E-01	AL161589.2	NT	Rattus norvegicus mRNA for alpha8 crystallin-related protein, complete cds
4889	17712	30317	0.96	2.4E-01	D00944.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5375	18175	30865	0.98	2.4E-01	A1925707.1	EST_HUMAN	Hepatitis C virus genomic RNA for polyprotein, complete cds
5376	18176	30866	0.98	2.4E-01	A1925707.1	EST_HUMAN	wc33d05.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	wc33d06.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2457129 3'
5569	18368	31275	8.16	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18368	31276	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5597	18392		0.77	2.4E-01	M63377.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5799	25076		0.90	2.4E-01	AJ133838.2	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' and
5805	18595	31520	2.22	2.4E-01	BF602336.1	EST_HUMAN	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
5896	18680	31627	3	2.4E-01	AF035546.1	NT	7f54d04.x1 NCI_CGAP_Br10 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5898	18780	31741	2.63	2.4E-01	7661801	NT	Q06170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
6050	18830	31793	0.67	2.4E-01	AV733787.1	EST_HUMAN	Drosophila melanogaster p38a MAP kinase gene, complete cds
6441	19209	32206	2.23	2.4E-01	A0698989.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
7243	19828	33004	9.5	2.4E-01	L43001.1	NT	AV733787 cDNA Homo sapiens cDNA clone cDAAD11 5'
7404	20081	33163	0.55	2.4E-01	N48732.1	EST_HUMAN	wc2c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7625	20291	33400	0.91	2.4E-01	AF229844.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
8247	20841	34078	1.61	2.4E-01	AJ012585.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
							Y55011.1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA clone IMAGE:277460 5'
							Mus musculus D3mxd48e protein (D3mxd48e) mRNA, complete cds
							Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8497	21189	34332	1.02	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
8552	21244		0.47	2.4E-01	BF078275.1	EST_HUMAN	602086189F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9030	21720	34874	0.49	2.4E-01	AL136077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9030	21720	34875	0.49	2.4E-01	AL136077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9463	22013	35181	7.01	2.4E-01	AI093515.1	EST_HUMAN	wd43602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains MER22.b1 TAR1 repetitive element;
9603	22256	35441	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9603	22256	35442	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22984	36202	1.68	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10667	23358	36598	4.8	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10739	23426	36671	1.39	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11158	23826		2.09	2.4E-01	Z21647.1	NT	P. aslettica mosaic: virus genomic RNA
11840	24424	37765	1.32	2.4E-01	BE617638.1	EST_HUMAN	601741421T1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3845836 3'
11801	24461	37801	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12019	25180		2.34	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12287	25162		1.97	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12400	25201		2.06	2.4E-01	BF184542.1	EST_HUMAN	601842848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4063739 5'
12720	24982		3.66	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
380	13187	25810	1.06	2.3E-01	S75896.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3168 nt]
622	13401		5	2.3E-01	U39743.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
652	13430	26069	33.31	2.3E-01	U67696.1	NT	Methanococcus jimaeschei section 138 of 150 of the complete genome
913	13680	26341	4.19	2.3E-01	BE311993.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505518 5'
1558	14305		1.12	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1599	14345	27035	1.23	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1628	14374	27063	2.74	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2038	14772		1.51	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2447	15166	27803	2.66	2.3E-01	BE297718.1	EST_HUMAN	601175582F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2657	15367	28105	1.59	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2827	14114	26789	3.38	2.3E-01	AB015033.1	NT	Marinifilabilia aquarvarans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2963	15729	28379	1.36	2.3E-01	AA001379.1	EST_HUMAN	no16006.s1 NCI_CGAP_Pha1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3363	16122	26780	1.14	2.3E-01	H69836.1	EST_HUMAN	Y97H10.1 Sources fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:213283 5'
3821	16573	29205	1.01	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3914	16964		5.22	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4316	17055	29680	1.1	2.3E-01	R8252.1	EST_HUMAN	Y17101.1 Sources placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4368	17106		1.98	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4417	17163	29784	1.03	2.3E-01	D90899.1	NT	Synectocystis sp. PCC6803 complete genome, 1/27, 1-133859
4454	17190	29816	2.51	2.3E-01	AF082535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4517	17252	29837	6.19	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4988	17711	30316	0.84	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5221	18028	30654	2.53	2.3E-01	AB040945.1	NT	Homo sapiens miRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.08	2.3E-01	BF068381.1	EST_HUMAN	7130606.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476899 3' similar to SW:GAG_SMSAV
5443	18242	31130	4.58	2.3E-01	X98587.1	NT	P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5563	18360		0.94	2.3E-01	L39112.1	NT	C.familiaris rom1 gene
5665	18460	31374	0.76	2.3E-01	S60371.1	NT	Vitis vinifera corneum small subunit ribosomal RNA gene
5851	18638	31575	1.50	2.3E-01	A1708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnosum, Genomic, 2806 nt]
5851	18638	31575	1.50	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
5851	18638	31575	1.50	2.3E-01	A1708840.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5851	18638	31575	1.50	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
5851	18638	31575	1.50	2.3E-01	A1708840.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6558	19323	32330	0.83	2.3E-01	AF108089.1	NT	Oryctolagus cuniculus cytochrome c oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	as42F12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318837 3' similar to contains Alu repetitive element
7011	19703	32759	1.08	2.3E-01	8023323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7188	19874	32947	0.9	2.3E-01	AF000227.1	NT	Seoale cereale oryzae secalin gene, complete cds
7315	19968	33077	3.14	2.3E-01	AF176389.1	NT	Glycine max testis linc protein LM17 precursor RNA, partial cds
7318	20001	33079	0.84	2.3E-01	AV719881.1	EST_HUMAN	AV719881 GLC Homo sapiens cDNA clone GLCDB08 5'
7318	20001	33080	0.84	2.3E-01	AV719881.1	EST_HUMAN	AV719881 GLC Homo sapiens cDNA clone GLCDB08 5'
7508	20179		2.94	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
7513	20184	33278	1.38	2.3E-01	BE888071.1	EST_HUMAN	60151157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7652	20316		2.73	2.3E-01	N80983.1	EST_HUMAN	aa12a08.1 Sources fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:292358 5'
7760	20446	33569	0.71	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58

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Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20587	33717	2.16	2.3E-01	M68931.1	NT	Oxytricha nova micronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57099.1	NT	Mus musculus proapoptin (pasp/SGP-1) gene, complete cds
8871	21363	34510	0.58	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NCL_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2891554 3'
8786	21478	34627	0.45	2.3E-01	AW804480.1	EST_HUMAN	EST370533 MAG3E resequences, MAGH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368)
9039	21729	34884	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368)
9480	22133	35313	0.62	2.3E-01	0679318	NT	Mus musculus phosphatidylcholine 3-kinase catalytic subunit delta (Plk3cd), mRNA
9609	22262	35448	0.62	2.3E-01	U77974.1	NT	Tribolium castaneum transcription factor homolog (To-ese) gene, complete cds
9628	22281	35471	0.5	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2866739 5'
9682	22334	35528	0.59	2.3E-01	AW604460.1	EST_HUMAN	EST376533 MAG3E resequences, MAGH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9767	22418	35625	0.59	2.3E-01	AW304633.1	EST_HUMAN	PM2-DT0036-281298-001-404 DT0036 Homo sapiens cDNA
9834	22485	35686	2.45	2.3E-01	BE179080.1	EST_HUMAN	MRO-HT0550-247400-014-g11 HT0550 Homo sapiens cDNA
9892	22542	35734	2.75	2.3E-01	AJ289281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10340	22987	36206	0.84	2.3E-01	AF201929.1	NT	Marine hepatitis virus strain 2, complete genome
10351	22988		5.11	2.3E-01	BF133577.1	EST_HUMAN	601849155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102082 3'
10937	23617	36887	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23617	36898	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 84 of the complete genome
11815	24403		1.75	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11855	24439		1.33	2.3E-01	8006010	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12088	24583		4.88	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M8 Homo sapiens cDNA clone HCCdE4 5'
12120	24612		1.62	2.3E-01	AW683940.1	EST_HUMAN	PM4-SN0012-03C400-001-608 SN0012 Homo sapiens cDNA
12173	25319	30711	2.88	2.3E-01	AW303623.1	EST_HUMAN	xx21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
12206	25368	30613	8.93	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2 ; contains PTR5.b2 TAR1 repetitive element ;
12255	24701		2.51	2.3E-01	BF683319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
						EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12303	24728		2.35	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12398	24784		1.76	2.3E-01	U49045.1	NT	Plutodites walli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12647	24952		2	2.3E-01	BF475611.1	EST_HUMAN	ner38h12.x1 Lujeldi, sciatic, nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element;
88	12914	25552	1.63	2.2E-01	AJ052190.1	EST_HUMAN	oz14a10.x1 Sox10, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1675200 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1557	14304	26983	1.64	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2082	14814	27547	2.52	2.2E-01	M34840.1	NT	Fresh-water spot type Emf1 alpha collagen (COLF1) gene
2402	15123	27860	6.3	2.2E-01	BF677538.1	EST_HUMAN	602086608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
2594	15308	28044	2.02	2.2E-01	BE182558.1	EST_HUMAN	601462629F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866180 5'
2594	15308	28045	2.02	2.2E-01	BE182558.1	EST_HUMAN	601462629F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866180 5'
2884	15851	28294	4.36	2.2E-01	BE156825.1	EST_HUMAN	PM2-HT0353-281299-003-#12 HT0353 Homo sapiens cDNA
2884	15851	28295	4.36	2.2E-01	BE156825.1	EST_HUMAN	PM2-HT0353-281299-003-#12 HT0353 Homo sapiens cDNA
2921	15887		1.57	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHIT) gene, exon 5
3387	16146		1.97	2.2E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3794	16546		1.12	2.2E-01	AF155728.1	NT	Xiphophorus malinatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4105	16848		0.72	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4194	16835	29562	6.45	2.2E-01	AF155142.1	NT	Mus musculus mibed kinase 3 (Mik3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4232	16973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4232	16973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meck1) mRNA, complete cds
4323	17062	29689	1.21	2.2E-01	U01307.1	NT	Human scRNA (hsc200 beta) pseudogene
4323	17062	29690	1.21	2.2E-01	U01307.1	NT	Human scRNA (hsc200 beta) pseudogene
4775	17507		1.36	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP6) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211216.1	EST_HUMAN	z087c05.1 Stratigene hNT neuron (#897233) Homo sapiens cDNA clone IMAGE:048908 5'
4982	17705		1.1	2.2E-01	L13200.1	NT	Mus musculus vinculin gene, exon 3
5082	17781		0.93	2.2E-01	S57565.1	NT	histamine H2-receptor [rata, Genomic, 1928 nt]
5140	17858	30474	2.64	2.2E-01	583597.4	NT	Vicia chalybeata mitochondrion, complete genome
5659	18454	31388	2.07	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5689	18464		4.6	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
5910	18694	31645	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx7) mRNA, complete cds
5910	18694	31647	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx7) mRNA, complete cds

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6606	18369	32381	0.73	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukulin, complete cds
6926	19662	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7029	19721	32777	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter A TP-binding protein (stpA) genes, complete cds; and unknown genes
7029	19721	32778	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter A TP-binding protein (stpA) genes, complete cds; and unknown genes
7191	19877	32850	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7191	19877	32951	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7396	20066	33144	0.63	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7628	20294	33402	0.66	2.2E-01	AB024563.1	NT	Bacillus halodurans DNA, complete and partial cds, strain: C-125
7919	20614		2.04	2.2E-01	AF155143.1	NT	Mus musculus rin23-M1 gene, promoter region
7987	20682	33808	1.01	2.2E-01	Z49933.1	NT	E.coli sepA and sepB genes
8449	21141	34279	0.64	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
8794	21486	34632	3.53	2.2E-01	AE001713.1	NT	Thermobia meridiana section 25 of 198 of the complete genome
8920	21611		4.35	2.2E-01	AW856039.1	EST_HUMAN	PM3-CT0263-241298-009-b07 CT0263 Homo sapiens cDNA
9013	21703	34853	1.45	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drocephila) (Deaf1), mRNA
9098	21786	34952	1.04	2.2E-01	BF376354.1	EST_HUMAN	MY1-TN0045-113900-006-c02 TN0045 Homo sapiens cDNA
9189	21859	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	zsf408.1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:281591 5'
9207	22086	35259	13.43	2.2E-01	P49634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9252	21931	35104	0.69	2.2E-01	AJ009639.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xkdp3)
9263	22017	35185	0.81	2.2E-01	7667428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9276	22030	35200	3.95	2.2E-01	M80643.1	NT	Brachydanio rerio opendymin beta and gamma chains (Epd) gene, complete cds
9521	22174	36358	0.58	2.2E-01	Q80980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CHG-3) (CNG3)
9716	22366	36564	3.4	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-sHSP21) mRNA, complete cds; nuclear gene for chloroplast product
9853	22503	35703	1.85	2.2E-01	BF206507.1	EST_HUMAN	601866724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10078	22724	35841	0.95	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10232	22880	36092	0.5	2.2E-01	T59472.1	EST_HUMAN	y663d08.r1 Stratiagene ovary (y6637217) Homo sapiens cDNA clone IMAGE:75855 5'
10232	22880	36093	0.5	2.2E-01	T59472.1	EST_HUMAN	y663d08.r1 Stratiagene ovary (y6637217) Homo sapiens cDNA clone IMAGE:75855 5'
							Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+-dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthase A (pqoA) genes, complete cds; and pyrodoquin>
10268	22816	36126	0.58	2.2E-01	AF068264.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10341	22888		0.61	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10387	23033	36247	0.6	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.6	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23168	36394	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.58	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.46	2.2E-01	AB021063.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11399	24005	37309	4.83	2.2E-01	X01918.1	NT	Drosophila 68C plus gene cluster
11438	23205	36437	5.22	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC61680), mRNA
11935	24493		1.66	2.2E-01	BE870869.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (GALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Lp
12040	25380		2.21	2.2E-01	U82671.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12123	24615		2.19	2.2E-01	AF188943.1	NT	
12225	17904	30591	3.87	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12228	24681		1.8	2.2E-01	AW661922.1	EST_HUMAN	h17002.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2972523 3'
12731	28371		2.58	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKG Homo sapiens cDNA clone GKGAHB02 5'
950	13716	26382	2.12	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lj2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26384	0.77	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1102	13859		2.76	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1176	13929	26593	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (linear2), mRNA
1176	13929	26594	1.15	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (linear2), mRNA
1906	14643	27353	2.07	2.1E-01	AA906824.1	EST_HUMAN	dk73602.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2152	14882	27616	4.2	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2485	15396	27942	1	2.1E-01	H739988.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247603 6'
2485	15596	27943	1	2.1E-01	H739988.1	EST_HUMAN	y004f07.at Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2556	15270	28005	0.91	2.1E-01	AF022814.1	NT	y004f07.at Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
							Fugu rubripes transcription factor (SLP-1) and homeobox gene, complete cds
2925	15891	28335	2.3	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3786	16538		6.08	2.1E-01	8638361	NT	Beta vulgaris mitochondrion, complete genome
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082		1.77	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4537	17272	29804	1.23	2.1E-01	AB010273.1	NT	Homo sapiens pslp47 gene, complete cds
5013	17734	30341	1.4	2.1E-01	Q01336	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2AAR)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6090	17809	30425	1.09	2.1E-01	AE001528.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218	18028	30650	0.24	2.1E-01	BF072865.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
6787	19531	32559	1.4	2.1E-01	AJ223392.1	NT	Dodo fragilis mitochondrial 16S rRNA gene, partial
6798	19469	32481	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7308	19889	33065	0.65	2.1E-01	Q01856	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7306	19889	33066	0.65	2.1E-01	Q01856	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000		2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7606	20272	33380	1.94	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7651	20315	33425	1.22	2.1E-01	AF068887.1	NT	Glycine max maleate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7651	20315	33426	1.22	2.1E-01	AF068887.1	NT	Glycine max maleate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7971	20688		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8400	21093	34229	4.44	2.1E-01	U88399.1	NT	Haemophilus influenzae hmdD, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds
8696	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8696	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
8857	21548		0.45	2.1E-01	AB022624.1	NT	Homo sapiens AFGL gene, exon 9
8936	21628	34788	5.68	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9404	22066	35237	0.57	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:270854 5'
9404	22066	35238	0.57	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:270854 5'
9413	22091	35262	2.31	2.1E-01	X97378.1	NT	A.thellena mRNA for AtrantBP1b protein
9518	22171	35354	1.13	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22875	36088	1.47	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10258	22906	36116	2.5	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
10264	22912	36122	0.97	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11554	24153		2.19	2.1E-01	11038647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
11870	24944		1.38	2.1E-01	X57824.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12377	24775		2.07	2.1E-01	AF217490.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12578	25287		1.47	2.1E-01	L32588.1	NT	Human granulins gene
12635	24935		1.42	2.1E-01	BE022149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12758	25019	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a50e02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	25650	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avana, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGL-18 protein (LOC51008), mRNA
683	13458	26103	1.24	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
792	13564	26225	2.19	2.0E-01	AF027866.1	NT	Mus musculus Major Histocompatibility Locus class II region
991	13753	28414	1.09	2.0E-01	D90906.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920916
1103	13880	28519	2.47	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1232	13981	28651	1.77	2.0E-01	AJ132895.5	NT	Homo sapiens rnc1 gene
1285	14035	28708	1.63	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-231289-002-c06 HT0422 Homo sapiens cDNA
1443	14180		1.52	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1470	14217	28804	14.63	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1544	14290	28977	1.97	2.0E-01	AB007674.1	NT	Homo sapiens rRNA, chromosome 1 specific transcript KIAA0505
1650	14296	28983	1.01	2.0E-01	AF260700.1	NT	Homo sapiens sodium/folate symporter mRNA, partial cds
1692	14436	27132	1.4	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1712	14455		1.67	2.0E-01	AF111170.3	NT	Homo sapiens 1-q32. Jagged2 gene, complete cds; and unknown gene
1752	14494		4.33	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1883	14620	27329	1.12	2.0E-01	BE871330.1	EST_HUMAN	001449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1883	14620	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	001449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	X82677.1	NT	H. sapiens Net-D-glucose cotransport regulator gene
							xp15b02.x1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	MER21 repetitive element ;
3683	16447	29087	0.89	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3822	16574	29206	1.12	2.0E-01	AL163204.2	NT	Homo sapiens cf chromosome 21 segment HS21C004
3936	16886	29327	0.78	2.0E-01	Z46906.1	NT	Sus scrofa
4628	17263		8.49	2.0E-01	BE926165.1	EST_HUMAN	QV4-EN0032-197600-223-a03 EN0032 Homo sapiens cDNA
4979	17702	30309	5.26	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
							HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5009	18237	28893	0.8	2.0E-01	P46607	SWISSPROT	
5359	18161	30845	2.63	2.0E-01	X56800.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5655	18450	31363	1.94	2.0E-01	11432540	NT	Homo sapiens dual adenosine-like domains 2 (DUOX2), mRNA
5750	18542	31464	0.76	2.0E-01	X91866.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
5969	18751	31712	6.3	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6081	18860		0.73	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6192	18968	31943	0.78	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6335	19105	32094	3.2	2.0E-01	X61033.1	NT	M.auratus mu class glutathione transferase gene
6435	19203	32200	4.02	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141098-001-g08 CT0247 Homo sapiens cDNA
7194	19880	32954	1.28	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkf) gene, exons 3 through 7
7345	20028	33102	0.68	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR
7676	20339	33452	0.84	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7853	20548		5.8	2.0E-01	AF028026.1	NT	Andes virus strain OI23133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33925	2.95	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8624	21316		0.99	2.0E-01	BE662247.1	EST_HUMAN	601344948F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677784 5'
9251	21630	35103	0.82	2.0E-01	U82511.1	NT	Dictyostelium discoideum random slug cDNA19 protein (rec19) mRNA, partial cds
9290	21957	35129	0.68	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9456	22006		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9646	22298	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146862.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22589	35792	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22589	35783	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10067	22715	35933	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10067	22715	35934	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22762		0.69	2.0E-01	X76388.1	NT	D.melanogaster DNA mobile element (hoppe)
10305	22952	36167	2.78	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
10744	23431	36674	1.58	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
10744	23431	36675	1.58	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11609	24207	37530	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37531	1.4	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.51	2.0E-01	AF206637.2	NT	Pinophytes promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12545	25210		1.39	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12556	25139	30894	1.36	2.0E-01	AW975297.1	EST_HUMAN	EST1367405 MAGIE resequences, MAGN Homo sapiens cDNA
12594	24950	30985	3.58	2.0E-01	A023592.1	EST_HUMAN	o680a10.s1 Soeris testis NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12618	24824		2.68	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30878	1.87	2.0E-01	11528495	NT	Mus musculus fructosebismine 3 kinase (Fn3k), mRNA
108	12629		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
342	13143	25781	0.66	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	26058	1.43	1.9E-01	U32581.2	NT	Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds
641	13420	26059	1.43	1.9E-01	U32581.2	NT	Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	26066	6.97	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
649	13427	26066	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
965	13730		1.73	1.9E-01	7305180	EST_HUMAN	Mus musculus interleukin 2 receptor, gamma chain (IL2g), mRNA
1082	13840	28499	13.43	1.9E-01	AA358813.1	EST_HUMAN	EST87784 Fetal lung II Homo sapiens cDNA 5' end
1349	14097	26772	1.76	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2380	15102	27841	3.61	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2923	15689	28333	3.43	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2939	15704		5.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3002	15768	28417	0.95	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3390	16149	28803	4.26	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	R18467.1	EST_HUMAN	Y42F10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3818	16568	29199	1.33	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3973	16722	29356	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4063	16808	29438	1.28	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4206	16847	29573	1.09	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-2i0700-007-d04 FN0010 Homo sapiens cDNA
4950	17677		1.05	1.9E-01	AF223842.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	x728a07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5558	18355	31265	7.87	1.9E-01	AF127837.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5749	18541	31463	0.7	1.9E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5795	18586		2.56	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT23P4 Homo sapiens cDNA clone NT2RP4001328 5'
6235	19009	31985	0.75	1.9E-01	AI762391.1	EST_HUMAN	wf54f02.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394039 3'
6294	19067	32050	1.03	1.9E-01	AW148452.1	EST_HUMAN	x14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
6876	17952	30548	1.69	1.9E-01	R43212.1	EST_HUMAN	y90a12.a1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
6900	19638	32682	0.89	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
6900	19638	32683	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7160	19847	32917	0.62	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7391	20070	33149	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7436	20113	33201	3.11	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
7885	20580	33709	1.46	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8586	21278	34417	10.77	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8944	21536	34881	1.24	1.9E-01	M14588.1	NT	Marupial cat beta-globin gene mRNA, partial cds
8944	21536	34882	1.24	1.9E-01	M14588.1	NT	Marupial cat beta-globin gene mRNA, partial cds
9775	22426	36632	0.81	1.9E-01	AA912486.1	EST_HUMAN	ob8g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537508 3' similar to contains Alu repetitive element
10142	22790	36006	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-010700-022-A02 ET0082 Homo sapiens cDNA
10142	22790	36008	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-010700-022-A02 ET0082 Homo sapiens cDNA
10540	23237	36470	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10540	23237	36471	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	36583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10986	23601	36915	1.34	1.9E-01	AA912480.1	EST_HUMAN	ob8002.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
10988	23691	36916	1.34	1.9E-01	AA912480.1	EST_HUMAN	ob8002.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537467 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
11487	24088	37369	1.53	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11726	24320	37845	2.77	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37673	1.6	1.9E-01	L07944.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12399	24785		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster cleftin light chain mRNA, complete cds
30	12858	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p118Rip mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022060.1	NT	Mus musculus Cdc gene for chaperonin containing TCP-1 gamma subunit, partial cds
361	13159	25802	1.76	1.8E-01	4502632	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	26158	1.01	1.8E-01	AB021460.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13726	26390	0.94	1.8E-01	AB012212.1	EST_HUMAN	wd71802.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1069	13826	26485	1.63	1.8E-01	AF000580.1	NT	Dictyostellium discoideum plasmid Ddp5, complete genome
1266	14015	26663	6.26	1.8E-01	AL117186.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26925	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26926	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1839	14577		1.2	1.8E-01	4503036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14597		1.58	1.8E-01	A1733708.1	EST_HUMAN	gg22d10.x5 NCI_CGAP_Kd13 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 075936 GAMMA BUTYROBETAINE HYDROXYLASE;

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14845	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya10-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2697	15406		2.36	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-08:1298-036-g04 DT0018 Homo sapiens cDNA
2898	15665		1.89	1.8E-01	AF184589.1	NT	Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds
2904	15670	28319	1.20	1.8E-01	AW182300.1	EST_HUMAN	X41a03.X1 Soariss NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859756 3'
3121	15886	28526	1.76	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3610	16363	29005	0.88	1.8E-01	H03369.1	EST_HUMAN	Y45601.s1 Soariss placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3610	16363	29006	0.88	1.8E-01	H03369.1	EST_HUMAN	Y45601.s1 Soariss placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4298	17038		1.43	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4519	17254	29888	5.94	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 56
4721	17463	30087	2.9	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya10-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17486	30114	0.94	1.8E-01	X62179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4984	17707	30311	2.03	1.8E-01	AW814270.1	EST_HUMAN	MF3-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
4990	17722	30325	1.06	1.8E-01	AI792382.1	EST_HUMAN	en28g07.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5035	17754	30367	4.68	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 90
5835	18624	31558	0.68	1.8E-01	N28629.1	EST_HUMAN	Y38H08.r1 Soariss melanocyte 2NtHM Homo sapiens cDNA clone IMAGE:264063 5'
6037	18817	31777	1.18	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6037	18817	31778	1.18	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6419	19187	32185	1.15	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6463	19230		2.06	1.8E-01	N94853.1	EST_HUMAN	Y62H02.r1 Soariss multiple sclerosis_2NtHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6906	19644	32689	1.18	1.8E-01	AB018501.1	NT	Citullus lanatus mRNA for wsus, complete cds
6906	19644	32690	1.18	1.8E-01	AB018501.1	NT	Citullus lanatus mRNA for wsus, complete cds
7346	20027	33103	0.7	1.8E-01	AP001611.1	NT	Bacillus halodurans genomic DNA, section 5/14
9242	21921	35091	1.23	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9274	22028	35198	1.22	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9391	22053		0.5	1.8E-01	AA493751.1	EST_HUMAN	h02a05.s1 NCJ CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element
9473	22126	35305	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22126	35306	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	0.91	1.8E-01	M28019.1	NT	S.commune oroliline-5'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	M28019.1	NT	S.commune oroliline-5'-phosphate decarboxylase (URA1) gene, complete cds
9679	22331	35528	0.75	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9863	22335	35530	0.77	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10033	22881		0.78	1.8E-01	AF200252.1	NT	Aquarius ampullus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10266	22914	36124	1.48	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	36465	3.08	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10637	19844	32689	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for virus, complete cds
10637	19844	32690	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for virus, complete cds
10638	23329	36567	5.69	1.8E-01	AF019107.1	NT	Dichostelium discoideum unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11767	24358	37691	3.45	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11967	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156318 5'
12476	24839		3.28	1.8E-01	Q96892	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	y48h10.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E.coli mRNA for hexokinase (hck1)
12745	25324		1.61	1.8E-01	X10695.1	NT	Rattus norvegicus CaBP6k gene
563	13345	25972	1.57	1.7E-01	BE385104.1	EST_HUMAN	601274804F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
787	13559	26221	2.32	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1036	13796	26455	1.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1036	13796	26456	1.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1974	14710		2.6	1.7E-01	AF255051.1	NT	Homo sapiens BNI(P3H (BNIP3H)) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28275	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpx) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2883	15631	28278	2.29	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15683	28338	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cix-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra cix-1 gene, exons 1-3
3103	15868	28508	1.24	1.7E-01	AF081514.1	NT	Taous canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ289505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3595	16348	28869	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3616	16389		0.92	1.7E-01	5031888	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16668	29308	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4522	17257		1.99	1.7E-01	X52836.1	NT	Schistosoma grigera alpha repetitive DNA
4787	17518	30140	1.06	1.7E-01	AJ247635.1	EST_HUMAN	qh57e09.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (se) gene, complete cds
5122	17840	30456	0.75	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18126	30785	2	1.7E-01	AA470688.1	EST_HUMAN	ne13a02.s1 NCI_OGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5323	18126	30786	2	1.7E-01	AA470688.1	EST_HUMAN	ne13a02.s1 NCI_OGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S
5608	18304	31205	0.62	1.7E-01	U43599.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6237	19011	31986	13.23	1.7E-01	H72118.1	EST_HUMAN	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6283	19068	32048	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19068	32049	0.97	1.7E-01	AJ370978.1	EST_HUMAN	ba29c11.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6753	17922	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	ba29c11.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6780	19524		2.28	1.7E-01	AF026552.3	NT	00084406771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880248 3'
6902	19640		0.88	1.7E-01	Z92910.1	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7120	19808	32874	1.1	1.7E-01	AP000422.1	NT	Homo sapiens HFE gene
7197	19883	32857	8.8	1.7E-01	BE734179.1	EST_HUMAN	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7380	20060	33139	1.37	1.7E-01	P16724	SWISSPROT	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 6'
7396	25112	33153	0.71	1.7E-01	Q01955	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
7760	20456	33580	1.32	1.7E-01	AF000573.1	NT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
							Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7863	20558	33684	0.82	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8175	20808	34001	6.19	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8175	20809	34002	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8598	21290	34431	0.47	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8628	21320	34462	2.09	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8743	21435	34580	0.76	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9068	21755	34918	0.48	1.7E-01	BE263142.1	EST_HUMAN	601116872F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9068	21755	34917	0.48	1.7E-01	BE263142.1	EST_HUMAN	601116872F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9490	22143	35323	7.85	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22250	35435	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 MAGE resequences, MAGO Homo sapiens cDNA
9597	22250	35436	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 MAGE resequences, MAGO Homo sapiens cDNA
9615	22268	35455	3.14	1.7E-01	U10288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22358	35555	0.63	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10293	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system), member 2 (SLC7A2), mRNA
10295	22942	36156	1.72	1.7E-01	AA827872.1	EST_HUMAN	h46067.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gb:L28081 TRANSFORMING PROTEIN RHOC (HUMAN);
10501	23147		0.45	1.7E-01	AL161642.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10579	23274	36511	8.78	1.7E-01	BE360835.1	EST_HUMAN	601288547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10709	23398	36637	2.65	1.7E-01	AA814617.1	EST_HUMAN	af43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
11055	23725	36985	9.13	1.7E-01	7105300	NT	Mus musculus adenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
11055	23725	36986	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
11146	23813	37098	1.62	1.7E-01	Y08391.1	NT	S.pombe pop1+ gene
11348	24038	37341	1.69	1.7E-01	AA883375.1	EST_HUMAN	a4509.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
11712	24307		1.83	1.7E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
11746	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
11746	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
11874	24453	37789	2.62	1.7E-01	11418157	NT	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12000	25320		1.95	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12268	25167		1.65	1.7E-01	AI824404.1	EST_HUMAN	ts69g05.x1 NCJ_CGAP_UH Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12552	24889	30998	16.27	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
122	12940	25582	2.38	1.6E-01	AF217532.1	NT	Homo sapiens invertebrate kinase gene, exon 6 and 7
664	15518	26081	1.51	1.6E-01	R31497.1	EST_HUMAN	Yi75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135598 5'
1493	14240	26927	1.16	1.6E-01	AA548863.1	EST_HUMAN	nk28d12.s1 NCJ_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1512	14268	26944	3.92	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1917	14654	27364	1.83	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1977	14713		1.51	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2383	15583	27844	1.35	1.6E-01	X64232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2497	15214	27957	1.4	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	15661	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2894	15661	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3624	16377	29019	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3682	16730		2.49	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4294	17033	29661	9.42	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4423	17159		3.07	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MA3E sequences, MAGJ Homo sapiens cDNA
4431	17167		4.35	1.6E-01	6763319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4869	17696	30219	0.7	1.6E-01	P40831	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4892	17619	30237	1.38	1.6E-01	AA088343.1	EST_HUMAN	z84h09.s1 Stratagene colon (#037204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4911	17639	30253	1.54	1.6E-01	AJ006356.1	NT	E221965 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4911	17639	30254	1.54	1.6E-01	AJ006356.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5303	18108	30768	0.99	1.6E-01	L40608.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5435	18234	30947	2.95	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5435	18234	30948	2.96	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5447	18246	31134	2.15	1.6E-01	AF034716.1	NT	HYPOTHETICAL_127.6 KD PROTEIN ;
5938	18720	31679	0.83	1.6E-01	BEQ25803.1	EST_HUMAN	xm43f01.x1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
6162	18939	31909	0.71	1.6E-01	BF183594.1	EST_HUMAN	HYPOTHETICAL_127.6 KD PROTEIN ;
6162	18939	31910	0.71	1.6E-01	BF183594.1	EST_HUMAN	xm43f01.x1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
							HYPOTHETICAL_127.6 KD PROTEIN ;
							Rattus norvegicus CCAAT/enhancer binding protein epsilon (cbbpe) gene, complete cds
							RC3-BN0034-31.0800-113-h01 BN0034 Homo sapiens cDNA
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6334	19104	32082	2.37	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6334	19104	32083	2.37	1.0E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6885	19802	32841	0.55	1.0E-01	AA398047.1	EST_HUMAN	z188d04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:729511 5'
6867	17944	30539	5.32	1.0E-01	AW291215.1	EST_HUMAN	U1-H.B12-egl-b-76-O.U1.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7676	20340	33453	1.66	1.0E-01	AW246359.1	EST_HUMAN	2822248.5prtmv NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.0E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81	1.0E-01	L49346.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.0E-01	BE244087.1	EST_HUMAN	TCBAP1E0007 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP0007
8018	20713	33844	0.87	1.0E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cfaA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8530	21222	34364	0.88	1.0E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8725	21417	34561	0.83	1.0E-01	R13873.1	EST_HUMAN	yf80h08.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:28873 5'
8831	21523		0.59	1.0E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21561	34708	1.72	1.0E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
9009	21669		0.83	1.0E-01	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.0E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041189-011-H01 ST0200 Homo sapiens cDNA
9554	22207	35301	1.7	1.0E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
9589	22242		0.87	1.0E-01	BE159984.1	EST_HUMAN	PM2-HT0363-270100-004-F11 HT0363 Homo sapiens cDNA
10553	23249	36488	3.3	1.0E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111-189-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36845	1.59	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.0E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3181183 5'
11059	23729		4.28	1.0E-01	AF109084.1	NT	Plasmidium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23984	37298	7.28	1.0E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.26	1.0E-01	BF527237.1	EST_HUMAN	602039465F2 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177073 5'
11886	25331		1.84	1.0E-01	6879468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
12002	24538	37273	5.28	1.0E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12292	24721	31052	1.72	1.0E-01	L14933.1	NT	Rat convertase PCS mRNA, 5' end
12321	24740		1.5	1.0E-01	AW839711.1	EST_HUMAN	RGI-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12418	25149		287.78	1.0E-01	AB046310.1	NT	Cucumis sativus KS mRNA for anti-leucine synthase, complete cds
12574	24901		2.4	1.0E-01	AK024496.1	NT	Homo sapiens rRNA for FLJ00104 protein, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12661	24961		1.72	1.6E-01	AF287344.1	NT	Fuchsin hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12667	24973	30992	1.7	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12798	25046		1.52	1.6E-01	BF672698.1	EST_HUMAN	802152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
241	13050	25689	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-04/700-197-E05 HT0619 Homo sapiens cDNA
241	13050	25690	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-04/700-197-E06 HT0619 Homo sapiens cDNA
573	15517		9.31	1.5E-01	AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH08 5'
766	13539	26188	1.09	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.5E-01	AJ006735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1076	13833	26491	2.75	1.5E-01	AJ251895.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1091	13849		0.82	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13946	26610	1.42	1.5E-01	AW195516.1	EST_HUMAN	zn39d11.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2696085 3'
1252	14001	26668	2.96	1.5E-01	D26635.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1252	14001	26669	2.96	1.5E-01	D26635.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1465	14212	26901	1.86	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1901	14638	27347	1	1.5E-01	AW44451.1	EST_HUMAN	UI-HB3-akb-b-09-0-UJ.at NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2716	15423	28162	1.98	1.5E-01	BF695381.1	EST_HUMAN	802083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2914	15690		1.16	1.5E-01	AW672616.1	EST_HUMAN	zw58d02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:U55072_ma1
3048	15814	28459	0.74	1.5E-01	Q78687	SWISSPROT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3347	16106	28761	5.06	1.5E-01	AA835049.1	EST_HUMAN	0068d05.at NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3361	16120	28777	0.82	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN); L. stagnalis mRNA for G protein-coupled receptor
3361	16120	28778	0.82	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3738	16491	29126	2.11	1.5E-01	U09904.1	NT	Mus musculus K2R/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3752	16504	29140	0.74	1.5E-01	7108358	NT	Homo sapiens p.ruvete dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3848	16599	29236	2.85	1.5E-01	AW665683.1	EST_HUMAN	h110f03.x1 Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2961411 3'
4028	16773	29405	1.1	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-161089-012-c08 HT0149 Homo sapiens cDNA
4161	16901	29530	8.35	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4676	17410	30046	1.57	1.5E-01	BF697695.1	EST_HUMAN	802067182F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4060223 5'
4703	15423	28162	1.92	1.5E-01	BF695381.1	EST_HUMAN	802083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5132	17850	30467	1.56	1.5E-01	Z72608.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL086w

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5146	17864	30480	1.05	1.5E-01	AF06313.1	NT	Morone saxatilis gonadotropin-releasing hormone type II gene, complete cds
5175	17864	30489	2.16	1.5E-01	P07896	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	AF268652.1	NT	Calman erododius MHC class II beta chain (hclbeta) gene, complete cds
5245	18051		0.92	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5451	18250	31139	5.08	1.5E-01	AW850754.1	EST_HUMAN	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5492	18281	31188	8.42	1.5E-01	U65016.1	NT	IL3-CT0219-163200-064-F10 CT0219 Homo sapiens cDNA
5492	18281	31189	8.42	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5915	18700	31653	3.09	1.5E-01	8753659	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5915	18700	31654	3.09	1.5E-01	8753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5952	18734	31693	1.93	1.5E-01	AJ276505.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6102	18890	31847	3.1	1.5E-01	BE727658.1	EST_HUMAN	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6152	18929		1.77	1.6E-01	4606398	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6251	19025	31989	2.09	1.5E-01	AF134907.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6409	25089	32176	2.21	1.5E-01	AE001039.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6437	19205	32201	4.99	1.5E-01	11417236	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6448	19216	32214	1.95	1.5E-01	P48508	SWISSPROT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6493	19259	32260	2.35	1.5E-01	Q28492	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6585	19348	32361	1.25	1.5E-01	AA714760.1	EST_HUMAN	AMELOGENIN
6612	19375	32380	1.86	1.5E-01	P30143	SWISSPROT	mw30d10.s1 NC1_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6682	17958	30554	6.82	1.5E-01	AW970295.1	EST_HUMAN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	EST382376 MAGC resequences, MAGK Homo sapiens cDNA
7115	18603		2.07	1.5E-01	AF210842.1	NT	db73102.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element
7290	19973	33051	2.86	1.5E-01	AF210842.1	EST_HUMAN	LTR2 repetitive element
7490	20162	33254	2.04	1.5E-01	AF299073.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7490	20162	33255	2.04	1.5E-01	AF299073.1	NT	wf52-08.x1 NC1_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7499	20171	33262	2.04	1.5E-01	AF299073.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33263	2.04	1.5E-01	AF299073.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33263	2.04	1.5E-01	AF299073.1	EST_HUMAN	UHF-BNO-akk-I-05-O-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	AW600911.1	EST_HUMAN	UHF-BNO-akk-I-05-O-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7957	20952	33775	0.96	1.5E-01	P21303	SWISSPROT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
							MEROZOITE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.a1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8211	20905		0.95	1.5E-01	BE884799.1	EST_HUMAN	801510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8299	20863		11.54	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5'
8332	21025	34162	1.6	1.5E-01	IL27835.1	NT	Panglossendon gigas growth hormone (GH) mRNA, complete cds
8491	21183	34325	1.65	1.5E-01	D84478.1	NT	Homo sapiens mRNA for ASK1, complete cds
8512	21204		0.71	1.5E-01	P43448	SWISSPROT	WNT-10A PROTEIN PRECURSOR
8737	21429	34575	1.16	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9002	21692	34842	2.88	1.5E-01	N7428.1	EST_HUMAN	za59a06.a1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:298886 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human;
9082	21781	34945	1	1.5E-01	BF585465.1	EST_HUMAN	GVO000404 Human Psoalis Differential Display Homo sapiens cDNA
9100	21788		2.3	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAB12 5'
9305	21972		0.74	1.5E-01	AU130007.1	EST_HUMAN	AU130007 NT2P3 Homo sapiens cDNA clone NT2RP3000080 5'
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
9717	22368	35596	0.53	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9821	22472	35674	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
9821	22472	35675	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10103	22751	35985	2.92	1.5E-01	X98852.1	NT	P. leniusculus mRNA for integrin beta subunit
10207	22855	36070	2.16	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10207	22855	36071	2.16	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10285	22833	36148	2.01	1.5E-01	U40892.1	NT	Danio rerio transcription factor Pac9b (Pac9) mRNA, complete cds
10438	23084	36311	1.43	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10438	23084	36312	1.43	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10595	23289	36526	1.62	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-21 0300-122-f11 BT0688 Homo sapiens cDNA
10595	23289	36527	1.62	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-21 0300-122-f11 BT0688 Homo sapiens cDNA
10726	23414	36654	7.31	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10726	23414	36655	7.31	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10896	23576		1.7	1.5E-01	AB042875.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
11012	23684	36944	1.6	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-DD4 CN0024 Homo sapiens cDNA
11057	23727	36998	1.95	1.5E-01	AA425488.1	EST_HUMAN	zw46c02.r1 Soares fetal_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11119	19973	33051	1.56	1.5E-01	A1973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11625	24222		1.56	1.5E-01	A1193704.1	EST_HUMAN	q972e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
11959	25202		11.07	1.5E-01	BF700582.1	EST_HUMAN	gb:M17887.008 ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12320	24739		1.37	1.5E-01	AF030358.2	NT	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12324	24743		1.77	1.5E-01	A1238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
							Mus musculus mRNA for death inducer-obliterator-1 (Dio-1)
12369	24771		5.35	1.5E-01	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12385	25220		9.97	1.5E-01	R83077.1	EST_HUMAN	y987e04.r1 Soares_fetal_liver_spleen_1N1FLS Homo sapiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA04 5'
12573	25150	30897	9.2	1.5E-01	AL136074.2	NT	Campylobacter jejuni NC1011168 complete genome; segment 1/6
12763	25036	30805	1.89	1.5E-01	AJ278242.1	NT	Sus scrofa mRNA for sodium iodide symporter
292	13098		1.72	1.4E-01	AF000863.1	NT	Homo sapiens T-cell receptor beta locus, TCRBV8SGP to TCRBV21S2A2 region
890	13659		3.82	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1236	13985		2.48	1.4E-01	T9184.1	EST_HUMAN	y954c01.s1 Soares_fetal_liver_spleen_1N1FLS Homo sapiens cDNA clone IMAGE:112032 3'
1742	14484		1.5	1.4E-01	6679880	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27186	1.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1898	14635		0.96	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-act-a-05-O-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1978	14714		9.33	1.4E-01	AA720815.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2478	15196	27836	1.38	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2795	15500	28241	4.23	1.4E-01	A1833496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3879	16629	29267	0.96	1.4E-01	R59232.1	EST_HUMAN	y997a03.r1 Soares_fetal_liver_spleen_1N1B Homo sapiens cDNA clone IMAGE:41467 5'
3879	16629	29268	0.86	1.4E-01	R59232.1	EST_HUMAN	y997a03.r1 Soares_fetal_liver_spleen_1N1B Homo sapiens cDNA clone IMAGE:41467 5'
4153	16895	29524	8.69	1.4E-01	A1698094.1	EST_HUMAN	b58c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4153	16895	29525	8.69	1.4E-01	A1698094.1	EST_HUMAN	b58c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16963	29577	3.73	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
5014	17735	30342	0.94	1.4E-01	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30656	5.48	1.4E-01	T80677.1	EST_HUMAN	y915c11.s1 Stratigene lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
6246	18052	30679	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5246	18052	30680	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6205	18980	31959	3	1.4E-01	BC326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6391	19180	32160	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19180	32161	5.8	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6460	19257		1.64	1.4E-01	BE296536.1	EST_HUMAN	601193523F11H_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6509	19274	32275	2.45	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-030300-103-409 UM0036 Homo sapiens cDNA
7026	19718		0.65	1.4E-01	AL118568.1	EST_HUMAN	DKFZp781A0910.J1 761 (synonym: harny2) Homo sapiens cDNA clone DKFZp781A0910 5'
7284	19987		1.51	1.4E-01	AW015373.1	EST_HUMAN	U1H-B10-east-c-19-D-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7521	20192	33283	1.19	1.4E-01	U85945.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7653	20317	33427	0.98	1.4E-01	AI305192.1	EST_HUMAN	q190b12.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8373	21068		1.23	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCF5H06 3'
8683	21375		0.57	1.4E-01	AI430063.1	EST_HUMAN	fr62b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to TR:002710 O02710 GAG POLYPROTEIN.
8811	21503	34950	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Cokin carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21583	34722	0.59	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Martin Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9021	21711	34864	0.97	1.4E-01	R62746.1	EST_HUMAN	y110h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	y110h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9085	21774	34838	8.81	1.4E-01	BF310959.1	EST_HUMAN	601895465F11H_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	W93411.1	EST_HUMAN	z194e04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER regulatory element:
9246	21925	35095	0.46	1.4E-01	X73293.1	NT	M. varnelli genes: rpoH, rpoB and rpoA
9246	21925	35096	0.46	1.4E-01	X73293.1	NT	M. varnelli genes: rpoH, rpoB and rpoA
9258	21937	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9268	21937	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.96	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22356	35551	0.97	1.4E-01	X68062.1	NT	C. parviflora ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023813.1	NT	Macromitrium levisium small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9988	22636	35846	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Martin Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9988	22636	35847	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Martin Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22805	36022	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-S10218-21 1299-013-408 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-S10218-21 1299-013-408 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84293.1	EST_HUMAN	y474d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10499	23145	36372	0.62	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
10607	23301		1.64	1.4E-01	AA811480.1	EST_HUMAN	oa99a03.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
10746	23433	36676	3.24	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2Nb1Bsd Homo sapiens cDNA clone IMAGE:154088 5'
10954	23031	36878	1.31	1.4E-01	AW104982.1	EST_HUMAN	xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11036	23707	36976	1.3	1.4E-01	T86102.1	EST_HUMAN	ye47g10.t1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120830 5'
11036	23707	36976	1.3	1.4E-01	T86102.1	EST_HUMAN	ye47g10.t1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120830 5'
11038	23709	36979	2.35	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD-10E)
11262	23924	37215	1.68	1.4E-01	X68092.1	NT	C. parvovirus ORF for putative membrane transport protein
11301	19867		1.41	1.4E-01	AW015373.1	EST_HUMAN	UI-H-810-aat-c-19-Q-UI.a1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11512	24112		1.82	1.4E-01	X52102.1	NT	M.musculus p70K gene for 10 kDa protein
11743	24335	37061	1.83	1.4E-01	AF146783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPnLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW664572.1	EST_HUMAN	h14h08.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872319 3'
11827	24411	37748	1.37	1.4E-01	AW664572.1	EST_HUMAN	h14h08.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872319 3'
12213	25172	30904	1.98	1.4E-01	AB000890.1	NT	Ephydria fluviatilis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P. salina plasmid gene secY
12275	24714		2.2	1.4E-01	11988117	NT	Rattus norvegicus deerin (Des), mRNA
12318	25393		2.84	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12413	24794		1.36	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2688767-3002965
12500	25407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		6.26	1.4E-01	D62983.1	NT	Mus musculus mRNA for prolidase, complete cds
12779	25033		2.37	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-22:1289-204-c08 HT0208 Homo sapiens cDNA
314	13118	25758	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25757	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25832	2.8	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
824	13594	26284	0.92	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13765	28425	1.31	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation



Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1105	13882		2.6	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1183	13945	26608	1.13	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAFF05 5'
1425	14172		1.18	1.3E-01	AF146277.1	NT	Homo sapiens alpha 1-antitrypsin mRNA, complete cds
1850	14588	27303	0.97	1.3E-01	6680957	NT	Mus musculus prolactin, type XI, alpha 1 (Ccl11a1), mRNA
1852	14687	27400	2.18	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14886		1.22	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acetylphosphate pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2288	15013		1.2	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2379	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15306	28042	4.76	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3065	15831	28474	1.01	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3443	16199	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3969	16718		1.43	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4137	16879		4.24	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-036-e03 DT0018 Homo sapiens cDNA
4145	16887	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	xc23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813865 3'
4257	16988	29827	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NP0 Homo sapiens cDNA clone NPDAZE02 5'
4257	16988	29828	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NP0 Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.76	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4497	17233	29863	2.68	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
4963	17688		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-183900-012-c06 TN0077 Homo sapiens cDNA
5242	18048	30877	0.83	1.3E-01	AW488888.1	EST_HUMAN	ha07b09.x1 NCJ_CGAP_K0412 Homo sapiens cDNA clone IMAGE:2872879 3' similar to contains L1.b1 L1
5278	18083	30739	2.23	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0063-100400-180-a08 UM0063 Homo sapiens cDNA
5414	18213		0.77	1.3E-01	AF107793.1	NT	Emmericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5497	18295		0.75	1.3E-01	AF066880.1	NT	Hepatitis C virus 58 CL10 genome polyprotein gene, partial cds
5638	18433	31346	0.97	1.3E-01	BF210820.1	EST_HUMAN	601874501F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5896	18981	31628	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5'
5896	18981	31629	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5'
6392	19161	32162	15.12	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6474	19241	32241	1.95	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6691	19608		0.75	1.3E-01	W26367.1	EST_HUMAN	26r3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6914	19661		0.99	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181866 5'
7162	19649		1.96	1.3E-01	H48064.1	EST_HUMAN	y33d02J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
7859	20554		0.88	1.3E-01	BE272339.1	EST_HUMAN	601126086F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
7873	20568	33694	1.34	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7802	20597	33727	1.17	1.3E-01	BF680652.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8136	20830		0.51	1.3E-01	BE562528.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3669634 5'
8172	20866	33998	0.64	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8243	20937		4.47	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
8285	20979		4.44	1.3E-01	8923919	NT	Homo sapiens cys histone macroH2A2.2 (MACROH2A2), mRNA
8426	21119	34258	1.02	1.3E-01	BF680652.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8847	21538	34683	0.58	1.3E-01	R11172.1	EST_HUMAN	y39g11J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8847	21538	34684	0.58	1.3E-01	R11172.1	EST_HUMAN	y39g11J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9119	21807	34973	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9119	21807	34974	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9372	21947	35120	3.71	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K-ATPase alpha 2c subunit mRNA, complete cds
9671	22323		0.56	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9951	22599		0.99	1.3E-01	8383940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10030	22678	35894	0.85	1.3E-01	AW851599.1	EST_HUMAN	MF2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10291	26128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36290	0.64	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10471	23117	36347	0.52	1.3E-01	AW247836.1	EST_HUMAN	2820637.3prine NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10528	23225		2.93	1.3E-01	BF330099.1	EST_HUMAN	MF4-BT0358-131700-010-h08 BT0358 Homo sapiens cDNA
10775	23458	36701	1.56	1.3E-01	H01883.1	EST_HUMAN	y32409.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11039	23710	36880	1.33	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23879		3.28	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11304	23963	37263	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23963	37264	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37504	4.26	1.3E-01	BE278449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11723	24317	37640	1.94	1.3E-01	BF616364.1	EST_HUMAN	601473369F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3876208 5'
11755	24346	37676	1.44	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12114	24607	31088	1.37	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868003 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12247	24685		4.43	1.3E-01	AJ242780.1	NT	Gallus gallus scyl1 gene for lymphocytin, exons 1-3
12274	24713		1.51	1.3E-01	Z13994.1	NT	R. norvegicus crp2 gene for cystatin related protein 2
12806	24915		1.43	1.3E-01	AB026829.1	NT	Ephydratia fluviatilis mRNA for sALK-6, complete cds
12836	24936		2.26	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares_Dieckgraeffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O61287 KIAA0539 PROTEIN.
374	13189	25844	8.42	1.2E-01	AM21744.1	EST_HUMAN	t39602.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
415	12826		1.06	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
534	13317		4.33	1.2E-01	AF039442.1	NT	Dicystostellum discoideum ORF DG1016 gene, partial cds
1366	14103	26778	3.22	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	14103	26779	3.22	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT23M4 Homo sapiens cDNA clone NT2RM4001691 3'
1362	14110		4.36	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT23M4 Homo sapiens cDNA clone NT2RM4001691 3'
1498	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1627	14379	27062	1.26	1.2E-01	Q14934	SWISSPROT	ak48608.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1490584 3' similar to TR:Q16871
1646	14392	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	Q16871 ANTHRUILLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.
1762	14504		20.17	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1913	14650		1.03	1.2E-01	AW449368.1	EST_HUMAN	q16809.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1980553 3'
2181	14910	27842	1.75	1.2E-01	BF248480.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2284	15009	27748	1.2	1.2E-01	AL163213.2	NT	UI-H-B13-aid-e-10-Q-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2697	15311	28047	1.49	1.2E-01	AW606566.1	EST_HUMAN	601821657F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4046224 5'
							Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-210300-120-f10 BN0046 Homo sapiens cDNA
							ta18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2229888 3' similar to TR:Q14048 Q14046
							COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element;
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	
2847	15616	28262	1.3	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2803	15689	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	ss80c09.x1 Bars lead cdon HPLURB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2835	15701	28350	2.92	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3004	15770	28418	0.97	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3224	15987	28641	1.89	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3252	16014		1.12	1.2E-01	U67800.1	NT	QV1-B10259-261099-021-c05 B10259 Homo sapiens cDNA
3472	16228		0.8	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3511	16267	28921	0.82	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2796131 to 3013640
							Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3611	16267	28022	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.46	1.2E-01	Z98118.1	NT	Bacillus subtilis complete genome (section 15 of 21) from 2795131 to 3013540
4160	18900	29528	1.97	1.2E-01	Z54255.1	NT	P. clarid mRNA; repeat region (ID 2MR17)
4160	18900	29529	1.97	1.2E-01	Z54255.1	NT	P. clarid mRNA; repeat region (ID 2MR17)
4672	17406	30041	1.1	1.2E-01	Z48183.1	NT	L. esculentum mRNA for glycylase-1
4739	17471		0.92	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5170	17979	30492	0.81	1.2E-01	AA744369.1	EST_HUMAN	my63c04.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5217	18025	30649	1	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5227	18034	30659	2.59	1.2E-01	W33035.1	EST_HUMAN	z08d02.r1 Soares_papillary thyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5284	18089	30749	2.3	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5419	18217	30828	0.68	1.2E-01	Z48234.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.93	1.2E-01	BE620945.1	EST_HUMAN	60149351B1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6153	18930	31898	1.36	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6206	18981	31960	2.35	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6337	19107	32097	0.57	1.2E-01	AA747535.1	EST_HUMAN	nc65c01.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6550	19315	32321	1.14	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
6700	19816	32658	0.59	1.2E-01	AF285739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20488		1.4	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-409 BN0137 Homo sapiens cDNA
7862	20557	33683	4.36	1.2E-01	A1913753.1	EST_HUMAN	wc98g03.x1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7906	20901	33731	0.67	1.2E-01	Q02369	SWISSPROT	Q90735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8208	20902	34037	0.73	1.2E-01	A1832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (Cl-B22)
							at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
8295	20989		10.29	1.2E-01	AW089652.1	EST_HUMAN	xc4c07.x1 NCJ_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2687597 3' similar to gb:M13452 LAMIN A (HUMAN);
8315	21008		3.34	1.2E-01	AF063772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8354	21047	34184	0.99	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8354	21047	34185	0.99	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8599	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

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8623	21315		0.62	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9471	22080	35252	2.93	1.2E-01	X77961.1	NT	S.cerevisiae HX15 gene
9906	22555	35750	1.59	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cl Hmo sapiens cDNA clone CUAKE08 5'
10611	23305	36543	1.38	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10801	23484		2.17	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10899	23672		3.18	1.2E-01	BE962324.2	EST_HUMAN	601655578RT NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
11094	23764		1.58	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11283	23944	37238	1.65	1.2E-01	R40249.1	EST_HUMAN	Y80C02.s1 Soanis Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11492	24093		1.67	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11892	24462		2.53	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12230	24683		3.52	1.2E-01	AJ271736.1	NT	Homo sapiens X1 pseudautosomal region; segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04912	SWISSPROT	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12417	24796		3.16	1.2E-01	AF188992.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntrophin gene, partial cds
12419	13317		3.19	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X53981.1	NT	R.norvegicus NF88 gene for 68kDa neurofilament
12586	25364	30611	1.44	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12610	24917	31007	5.88	1.2E-01	A1298903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1896840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	O98433	SWISSPROT	CYGLIN T
12663	24962	30989	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
12800	16228		1.81	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
12812	23372	30614	1.38	1.2E-01	9845282	NT	Mus musculus protein (18kDa) similar to human SYK interacting protein (p18K), mRNA
651	13334	25964	0.8	1.1E-01	AJ561003.1	EST_HUMAN	hm18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
601	13379	28010	1.65	1.1E-01	AA569006.1	EST_HUMAN	nm008111.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb.X06985_ma1
1032	13792	28452	2.03	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	13821		1.3	1.1E-01	AL161560.2	NT	602120847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1136	15561	29552	4.62	1.1E-01	AW1972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, config fragment No. 80
1227	13977	28648	3.01	1.1E-01	D64004.1	NT	EST384142 MACIE resequences, MAGL Homo sapiens cDNA
1511	14257	28943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002965
2312	15037		1.85	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA

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2540	15530		1	1.1E-01	6978678	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15286		1.17	1.1E-01	AW821809.1	EST_HUMAN	RCO-ST0379-21 0100-032-g04 ST0379 Homo sapiens cDNA
3030	15798	28442	0.82	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3338	18098		1.78	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca <sub>v</sub> 1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393186.1	EST_HUMAN	601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627086 5'
3444	16200	28850	1.21	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XX
3570	16325	28972	0.77	1.1E-01	Y07685.1	NT	A.limmerus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	29089	1.47	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4090	16833	29456	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-25 0100-025-g07 ST0280 Homo sapiens cDNA
4090	16833	29457	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-25 0100-025-g07 ST0280 Homo sapiens cDNA
4228	16867		8.78	1.1E-01	AF167066.1	NT	Drosophila melanogaster klaricht protein (klar) mRNA, complete cds
4254	16895	29624	0.77	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-02X1500-068-e08 UM0070 Homo sapiens cDNA
4594	17329	29956	0.96	1.1E-01	S44957.1	NT	Tape-1=Integral membrane protein TAPA-1 (mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7)
4780	17512	30134	1.2	1.1E-01	Y07685.1	NT	A.limmerus gene for transposase
4967	16839		0.85	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II (region:butyrophilin-like protein gene, partial cds; Notch4, PEX2, FIAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-PP, and tenascin X (TNX) genes, complete>
5077	17798	30412	1	1.1E-01	P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18381		1.4	1.1E-01	AA747216.1	EST_HUMAN	nc78603.s1 NCJ_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5653	18448	31361	1.23	1.1E-01	AF020827.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5687	18480	31369	0.88	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537	31459	1.81	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5781	18572	31500	5.31	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5936	18718	31676	1.67	1.1E-01	AJ007973.1	NT	Homo sapiens L3MD2B gene
5955	18737	31686	1.75	1.1E-01	BE769152.1	EST_HUMAN	PA3-FT0024-13 0600-004-f12 FT0024 Homo sapiens cDNA
5976	18757	31719	9.4	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0264-28 0899-011-e01 CT0264 Homo sapiens cDNA
6330	19100	32088	0.67	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338	19108	32098	1.25	1.1E-01	AF035748.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6381	19150	32149	0.72	1.1E-01	AI216307.1	EST_HUMAN	9g78606.x1 Soares_NFL_T_05C S1 Homo sapiens cDNA clone IMAGE:1841086 3'
6512	19277	32278	3.71	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6604	19367		3.03	1.1E-01	AF032822.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

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6897	19814	32865	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6948	19430	32445	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
6948	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7087	25423		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7203	25107	32964	0.84	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1160001-1485000 nt, position (9/7)
7435	20112	33199	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.93	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7595	20263	33371					ah31506.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
7688	20563	33690	3.35	1.1E-01	AA788784.1	EST_HUMAN	CHROMOGRAFIN A PRECURSOR (HUMAN);
8107	20801	33933	0.5	1.1E-01	U07492.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20801	33934	1.7	1.1E-01	AA493574.1	EST_HUMAN	nr04g10.s1 NCI_CQAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.7	1.1E-01	AA493574.1	EST_HUMAN	nr04g10.s1 NCI_CQAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X91233.1	NT	H. sapiens IL15 gene
8193	20887		1.14	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-030200-001-409 ST0270 Homo sapiens cDNA
8249	20943	34081	1.45	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P194.1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547P194 5'
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	Pedococcus acidilactici H1 plasmid pSMB174 pediocin AclH production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8810	21602	34649					wf48c01.x1 Soares_MFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
8908	21597	34739	0.86	1.1E-01	AI807474.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34775	0.47	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34775	2.04	1.1E-01	AA192153.1	EST_HUMAN	z963b12.r1 Striatagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8941	21632	34776	2.04	1.1E-01	AA192153.1	EST_HUMAN	z963b12.r1 Striatagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9033	21723	34877	0.74	1.1E-01	Y12727.1	NT	P. furiosus partial dph5 gene and argF gene
9063	21762	34912	2.04	1.1E-01	T72875.1	EST_HUMAN	y019h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9090	21779		0.6	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9322	21989		0.88	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271089-026-g11 HT0142 Homo sapiens cDNA
9396	22058		2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
9810	22461		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10017	22665		0.45	1.1E-01	BE315509.1	EST_HUMAN	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
10106	22764		1.57	1.1E-01	R80590.1	EST_HUMAN	y08a09.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:147064 3'
10235	22863	36096	1.26	1.1E-01	U80529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10708	15796	28442	2.05	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1102 3'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10840	23622		2.75	1.1E-01	AF169032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
10974	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	yh35f12.1 Soares placenta Nb2Hp Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
10983	23658	36911	1.39	1.1E-01	8081351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37079	1.58	1.1E-01	X70098.1	NT	M.musculus cytokine gene
11169	23838	37117	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11169	23838	37118	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11277	23938	37230	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24269		1.65	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11890	24529		1.36	1.1E-01	AA182153.1	EST_HUMAN	zp93b12.11 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12096	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-1 20600-014-f03 NT0112 Homo sapiens cDNA
12341	25180		1.97	1.1E-01	BE974558.1	EST_HUMAN	601806551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'
12750	25012	30977	3.15	1.1E-01	BF239753.1	EST_HUMAN	601806360F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1179	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13998	26685	2.63	1.0E-01	A1985489.1	EST_HUMAN	ws08d01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1371	14119	26704	1.95	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2493	15210	27952	1.11	1.0E-01	AW451365.1	EST_HUMAN	UI-H-B13-alc-d-17-Q-UI.s1 NCI CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2739420 3'
3503	16259	28913	1.19	1.0E-01	BF033907.1	EST_HUMAN	601456301F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855949 5'
3708	16461	29100	1.03	1.0E-01	BF239818.1	EST_HUMAN	601806489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16589	29200	0.96	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3817	16669	29201	0.98	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3835	16885	29328	2.53	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-190800-318-e05 NT0048 Homo sapiens cDNA
4518	17253		0.95	1.0E-01	A1792349.1	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4884	17398	30032	1.19	1.0E-01	U60450.1	NT	Drosophila melanogaster tyrosine kinase p45 lacform (far) mRNA, complete cds
4896	17594	30217	2.35	1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGE Homo sapiens cDNA
5238	18044		9.73	1.0E-01	W88490.1	EST_HUMAN	zh62h04.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:410695 3'
5789	18580		1.21	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
5934	18717	31675	14.15	1.0E-01	AF24875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6243	19017	31901	0.99	1.0E-01	AA481879.1	EST_HUMAN	zw41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains
6258	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	zu67c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924	19680		1.81	1.0E-01	R23821.1	EST_HUMAN	h34h06.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:131875 5' similar to contains Alu repetitive element
7635	20300		2.67	1.0E-01	Y12488.1	NT	M.musculus w1n gene
7709	20373	33486	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20529	33656	0.65	1.0E-01	AA861001.1	EST_HUMAN	ak32g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407896 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8098	20760		0.5	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.98	1.0E-01	AW189797.1	EST_HUMAN	x09b01.x1 NC1_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element;
9084	21773	34037	1.04	1.0E-01	AF102856.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapmon mRNA, complete cds
9395	22057	35228	0.51	1.0E-01	R44993.1	EST_HUMAN	y933h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.8	1.0E-01	M76729.1	NT	Human pro-alpha1(V) collagen mRNA, complete cds
9450	22000		3.02	1.0E-01	AE001801.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9464	22074	35245	0.75	1.0E-01	W01955.1	EST_HUMAN	zc66c10.s1 Soares fetal heart NIH#119W Homo sapiens cDNA clone IMAGE:327282 3'
9721	22372	35571	1.67	1.0E-01	BF240154.1	EST_HUMAN	601905861F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10048	22696	35912	0.51	1.0E-01	T51952.1	EST_HUMAN	y029a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10228	22877	36089	0.89	1.0E-01	BE782750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939086 5'
10554	23250		1.95	1.0E-01	AU169127.1	EST_HUMAN	AU159127 THYR01 Homo sapiens cDNA clone THYR01000895 3'
10958	23634	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10958	23634	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23983	37283	6.22	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11510	24110		1.52	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Salmonella-VT1) inserted region, substrain:RMD 0508952
11594	24193	37511	1.48	1.0E-01	Z71446.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11594	24193	37512	1.46	1.0E-01	Z71446.1	NT	A.thaliana mRNA for CLC-b chloride channel protein
11832	24410	37755	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
11832	24410	37756	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
12083	24921		4.32	1.0E-01	BE637719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12300	24725		1.71	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12317	24738		2.22	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12614	24821		2.74	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12677	26318		5.03	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25002		8.8	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15496	28224	1.27	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R11) mRNA, complete cds
2780	15495	28235	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2790	15495	28236	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3260	16022	28871	1.32	9.9E-02	AF090810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
3633	16883	28324	0.75	9.9E-02	A1821637.1	EST_HUMAN	zu45c03.x6 Soerenga ovary tumor NihOT Homo sapiens cDNA clone IMAGE:740932 3'
4632	17367	30003	0.93	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6875	17951	30547	9.17	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blebsidin S deaminase, complete cds
7815	20510	33634	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2566528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
7815	20510	33635	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2566528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9156	21887	35055	0.98	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O. sativa RAmY6/C gene for alpha-amyrase
3100	15865		0.9	9.8E-02	4504578	NT	Homo sapiens I factor (complement) (IF) mRNA
3142	15908	28550	3.04	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4198	16839	29564	6.24	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4198	16839	29565	6.24	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7361	20061		0.77	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9153	21894		1.18	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11437	23204	36436	2.05	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12052	24570		1.78	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1328	14077	26752	1.31	9.7E-02	AB005806.1	NT	Alice arborescens mRNA for NADP-malic enzyme, complete cds
1580	14326		1.49	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2257	14984	27724	2.08	9.7E-02	BE168900.1	EST_HUMAN	QV1-HT0516-07/300-095-s04 HT0516 Homo sapiens cDNA
3665	16714		3.48	9.7E-02	Q98795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18067	30695	0.94	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5261	18067	30896	0.94	9.7E-02	AF089189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5924	18708	31862	1.43	9.7E-02	AW954476.1	EST_HUMAN	EST386548 MAGC resequences, MAGC Homo sapiens cDNA
7198	19884	32958	3.24	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2987771 to 3213410
7882	20577	33705	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	A1853884.1	EST_HUMAN	wx78b06.x1 NC1 CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
11152	23819		2.84	9.7E-02	U58337.1	NT	PEPTIDYL-PRC1LYL CIS-TRANS ISOMERASE A (HUMAN);
2009	14744	27470	1.11	9.6E-02	AJ080721.1	EST_HUMAN	Mus musculus Iyath (Lqth) mRNA, partial cds
2009	14744	27471	1.11	9.6E-02	AJ080721.1	EST_HUMAN	oz47d11.x1 Soaree_NHMFu_S1 Homo sapiens cDNA clone IMAGE:1878485 3'
4311	17050	29875	5.8	9.6E-02	Z32686.2	NT	oz47d11.x1 Soaree_NHMFu_S1 Homo sapiens cDNA clone IMAGE:1878485 3'
4940	17968	30276	0.99	9.6E-02	AW966230.1	EST_HUMAN	Proteus mirabilis fibrinogen operon, strain HI4320
6014	18795		3.13	9.6E-02	BE910039.1	EST_HUMAN	EST378303 MAGC resequences, MAGI Homo sapiens cDNA
8274	20868		0.6	9.6E-02	AU137084.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9444	22121	35300	1.31	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9772	22423		1.12	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9839	22587	35790	1.29	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
9839	22587	35791	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22968	35884	0.5	9.6E-02	BF677270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10051	22969	35915	1.64	9.6E-02	AB013985.1	NT	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250989 5'
10051	22969	35916	1.54	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10158	22906	36024	3.35	9.6E-02	F08174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10643	23334	36572	7.22	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
12652	24954		3.34	9.6E-02	H14590.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
4081	18825	29452	2.1	9.5E-02	AW992395.1	EST_HUMAN	ym18h03.s1 Soaree Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5579	18376	31289	0.65	9.5E-02	F51854	SWISSPROT	CN42-BN0023-06:0200-087-f12 BN0023 Homo sapiens cDNA
6988	19881	32728	0.55	9.5E-02	AA780728.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7202	19888	32963	4.72	9.5E-02	AB003473.1	NT	sc88a09.s1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7467	20141	33234	7.68	9.5E-02	AL101538.2	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7597	18376	31289	0.84	9.5E-02	F51854	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7780	20476	33600	1.83	9.5E-02	BF036881.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7780	20475	33601	1.83	9.5E-02	BF036881.1	EST_HUMAN	601453642F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243 5'
10578	23273	36509	2.36	9.5E-02	BF036881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10578	23273	36510	2.36	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1825	14564	27275	2.82	9.4E-02	BF671063.1	EST_HUMAN	602150862F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1857	14595	27310	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14595	27311	0.99	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	16610	29249	4.43	9.4E-02	Z33059.1	NT	M. capricorn DNA for CONTIG MC073
6225	18998	31976	0.63	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8498	21190						
10851	20186	33258	2.46	9.4E-02	Z46863.1	NT	Acinetobacter sp. cydQ, cobQ, cobQ, sodM, lyeS, rubA, rubB, estB, oxyR, ppk, mltA, ORF2 and ORF3 genes
11941	25255		2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and p35 gene, partial cds
12671	24965		1.76	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
2988	15754		1.92	9.4E-02	AF188036.1	NT	Myeloplasma pulmonis hypodermal membrane protein P83 gene, complete cds
3028	15792		1.97	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3251	16013	28665	6.32	9.3E-02	6012525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
4132	16874	28502	1.95	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	29503	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4685	17419		3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
5576	18373		2.04	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
8146	20840	33972	0.87	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
9610	22263	35449	0.82	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
10091	22739	35853	2.15	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855681 3'
10091	22739	35854	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22866		3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
12194	25181		3.6	9.3E-02	AW206117.1	EST_HUMAN	UI-HB11-afx-h-c6-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12550	25209		2.51	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
			8.43	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12752	25254						Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bclg1 (BIN31), taxasin (taxasin), RafGDS-like factor (RUF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
222	13034	25668	2.1	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25669	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2224	14952		8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
3175	15638	28567	1.68	9.2E-02	R54156.1	EST_HUMAN	yg9807.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3299	16061	28708	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
			0.85	9.2E-02	AA534354.1	EST_HUMAN	mt79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3573	16328		1.28	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4213	16954		0.99	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4274	17013		0.78	9.2E-02	BE299722.1	EST_HUMAN	600944395F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
7907	20602	33732	1.88	9.2E-02	T46920.1	EST_HUMAN	y98009.t1 Stratiogene placenta (#637225) Homo sapiens cDNA clone IMAGE:68808 5' similar to
8076	20770	33898	2.2	9.2E-02	X95256.1	NT	gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
11895	24290	37614	1.27	9.2E-02	AF026552.3	NT	H. vulgare xylose isomerase gene
12738	25412		1.4	9.2E-02	11468872	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
414	12825	25439	4.19	9.1E-02	X77665.1	NT	Podospora anserina mitochondrion, complete genome
4451	17187	29812	1.33	9.1E-02	AL161554.2	NT	O. cuniculus K12 keratin gene
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5843	18438	31352	1.44	9.1E-02	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, Gdb, G6c, G5b, G6a, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TC7, LST-1, LTB, TNF, and LTA genes, complete cds
7285	19989	33045	14.94	9.1E-02	AW160858.1	EST_HUMAN	eu74605.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7575	20244	33349	0.78	9.1E-02	AF000061.1	NT	Aeropyrum pernix genomic DNA, section 47
7809	20275	33383	0.72	9.1E-02	X9073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
8822	21514	34659	0.88	9.1E-02	Y14378.1	NT	Homo sapiens gamma adducin gene, exon 9
10327	22974		1.37	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratiogene Homo sapiens cDNA clone FB19F10 3'end
10354	23001	36218	1.25	9.1E-02	S74059.1	NT	Tg618-Cyl actin [Tripeustes gratillae sea urchins, embryos, Genomic, 5275 nt]
10383	23029	36244	1.19	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12110	25348		1.4	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to
12181	24653		2.12	9.1E-02	AF052695.1	NT	SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12637	25204		1.93	9.1E-02	AJ291390.1	NT	Rattus norvegicus cell cycle protein p65CDC gene, complete cds
						NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
727	13501	26155	4.3	9.0E-02	P16328	SW/ISSPROT	h39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
1631	14377	27084	5.28	9.0E-02	BE220482.1	EST_HUMAN	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2806	15511	28252	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2806	15511	28253	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28744	0.84	9.0E-02	AF279135.1	NT	Dicystostellum discoideum spore coat structural protein SP65 (cdtE) gene, complete cds
4619	17354	29989	3.27	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5906	18391	31840	5.21	9.0E-02	W50037.1	EST_HUMAN	2a88a12.1 Soares_fetal_lung_NiHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6819	10381		1.14	9.0E-02	BF062651.1	EST_HUMAN	7h63d003.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
6868	19595	32819	0.72	9.0E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placentia NB214P Homo sapiens cDNA clone IMAGE:138903 3'
12486	24845		2.01	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CsdD (csdD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tr (tr), OrtU (ortU), >
1418	14100	20849	1.98	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1418	14186	26850	1.99	8.9E-02	BF701593.1	EST_HUMAN	PMO-HT0339-251199-003-001 HT0339 Homo sapiens cDNA
2386	15107	27846	1.22	8.9E-02	BE163572.1	EST_HUMAN	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4175	16915		1.93	8.9E-02	AF286055.1	NT	UI-H-B13-alo-f-03-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5780	18552	31474	3.22	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-03-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5780	18552	31475	3.22	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-03-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5776	18507	31496	3.39	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC33107), mRNA
7093	19782	32848	1.94	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7453	20132		2.06	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC0pA20F8
7849	20844	33768	1.08	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8030	20725	33858	0.72	8.9E-02	BF701685.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33859	0.72	8.9E-02	BF701685.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8496	21188	34331	4.72	8.9E-02	AA306319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9520	22173	35356	0.8	8.9E-02	A1285827.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ;
9620	22173	35357	0.8	8.9E-02	A1285827.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ;
9632	22284	35477	0.76	8.9E-02	AA339355.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11882	25173		1.49	8.9E-02	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
11940	25207		1.48	8.9E-02	P19624	SWISSPROT	MYOSIN-2 ISOFORM
12085	24591		3.05	8.9E-02	BF666918.1	EST_HUMAN	602129882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12284	24716		1.61	8.9E-02	U20905.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1352	14100	26775	1.59	8.8E-02	O27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3883	16933	29272	1.03	8.8E-02	AA298128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16780		3.55	8.8E-02	000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4214	16955		0.99	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4590423	NT	Homo sapiens paired box gene 6 (enkidia, keratins) (PAX6), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8888	21577	34719	1.07	8.8E-02	AA151872.1	EST_HUMAN	zn89a05.s1 Striatagene colon (#837204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11228	23891	37178	6.92	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24641	31088	2.66	8.8E-02	Z71551.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1642	14388	27077	1.15	8.7E-02	AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3681	16434	29077	3.66	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	16434	29078	3.66	8.7E-02	U62695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5231	18037	30683	5.89	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5231	18037	30684	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32612	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6745	19578	32613	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6943	19425	32440	0.71	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
7761	20457		0.45	8.7E-02	AA284532.1	EST_HUMAN	zt20e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10810	23304		2.46	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11282	23943	37237	2.55	8.7E-02	AJ007763.1	NT	Glucobacter oxydans rRNA-16S and rRNA-16S genes
12145	24633		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	8679057	NT	Mus musculus n dogen 2 (Nd2), mRNA
1230	13979	26849	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2240	14968	27706	1.82	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3183	15946	28596	4.57	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3635	16388		3.77	8.6E-02	AF153362.1	NT	Dicystotellum diisocitrate dehydrogenase (sdhA) gene, complete cds
5134	17862		0.86	8.6E-02	BF570296.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
6003	18784	31746	4.75	8.6E-02	Y10828.1	NT	Homo sapiens LCN1b gene
6281	19064	32033	1.58	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6281	19064	32034	1.50	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7481	20163	33248	1.34	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7831	20526	33651	1.25	8.6E-02	5730068	NT	Homo sapiens Sfr2-related CBP activator protein (SRCAP) mRNA
7831	20526	33652	1.25	8.6E-02	5730068	NT	Homo sapiens Sfr2-related CBP activator protein (SRCAP) mRNA
7989	20864	33788	0.82	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8031	20728		0.81	8.6E-02	U60168.1	NT	Dicystotellum diisocitrate dehydrogenase subunit C2 homolog PycC (pyrC) gene, complete cds
9637	22289	35482	1.76	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9673	22325		0.59	8.6E-02	AW962153.1	EST_HUMAN	h120c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10053	22701	35918	0.81	8.6E-02	AF028604.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
10865	23545	36792	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10865	23545	36793	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11214	23877	37163	4.04	8.6E-02	BF305606.1	EST_HUMAN	601883437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138216 5'
11214	23877	37164	4.04	8.6E-02	BF305606.1	EST_HUMAN	601883437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138216 5'
11417	23184	38414	5.97	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11588	24167	37481		8.6E-02	AF283890.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.6E-02	AE000852.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.6E-02	AA985491.1	EST_HUMAN	cc63b07.s1 NCI_CGAP_K046 Homo sapiens cDNA clone IMAGE:1582917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5821	18417		1.29	8.6E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5921	18708	31058	6.95	8.6E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8504	21196	34340	1.65	8.6E-02	5754779	NT	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35591	2.81	8.6E-02	BE833054.1	EST_HUMAN	RC4-OT0037-2c0700-014-405 OT0037 Homo sapiens cDNA
9736	22387	35592	2.81	8.6E-02	BE833054.1	EST_HUMAN	RC4-OT0037-2c0700-014-405 OT0037 Homo sapiens cDNA
10261	22309	36119	0.54	8.6E-02	X76731.1	NT	V. armodyles gene for armodytoxin C
10382	23028	36243	0.87	8.6E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF-5), mRNA
11105	23775		8.87	8.6E-02	AF155510.1	NT	Homo sapiens lipase precursor, mRNA, complete cds
11125	23794	37070	4.43	8.6E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12700	24981		3.8	8.6E-02	AA362334.1	EST_HUMAN	EST12736 Overy II Homo sapiens cDNA 6' end
2672	15602	28121	3.73	8.4E-02	W69330.1	EST_HUMAN	z444et1.1 Sources fetal heart NHF119W Homo sapiens cDNA clone IMAGE:343532 5'
3801	18553	29184	1	8.4E-02	A1827586.1	EST_HUMAN	wf10f11.x1 Sources NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSR1 repetitive element;
4321	17060	29685	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4321	17060	29686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042555.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5229	18035	30661	9.84	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6590	19353	32366	1.72	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7928	20623	33751	7.18	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0780-260400-162-d05 BT0780 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218890.1	NT	Homo sapiens titractin precursor (ATRIN) gene, exon 2
10280	22908	36118	1.83	8.4E-02	A1735184.1	EST_HUMAN	es88g10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
12070	24584	31122	1.68	8.4E-02	R79408.1	EST_HUMAN	y83h12.r1 Sources placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27465	0.92	8.3E-02	5835680	NT	bodles hexagonus mitochondrion, complete genome
2005	14741	27466	0.92	8.3E-02	5835680	NT	bodles hexagonus mitochondrion, complete genome
3580	18335	28980	6.91	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3607	18360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Sources NHMPu S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3607	18360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Sources NHMPu S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6166	18943	31914	1.05	8.3E-02	A1942338.1	EST_HUMAN	w079f11.x1 NC_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2461581 3'
6273	19046	32023	3.05	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7880	20575	33702	2.98	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
7911	20605		1.46	8.3E-02	AA855285.1	EST_HUMAN	og88g08.s1 NC_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1458422 3' similar to contains L1.H L1 L1
8198	20892		1.32	8.3E-02	AA987873.1	EST_HUMAN	repetitive element;
9438	22116	35291	1.41	8.3E-02	AW583503.1	EST_HUMAN	og81f10.s1 NC_CGAP_Kd6 Homo sapiens cDNA clone IMAGE:1592779 3'
9451	22001		1.88	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10240	22888		0.49	8.3E-02	AF020409.1	NT	Dicotyledonum di scodium Doca (dca) mRNA, complete cds
12158	25353		1.67	8.3E-02	BE958458.1	EST_HUMAN	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928863 5'
1357	14105		7.15	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1481	14228	26914	1.99	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3071	15837		2.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3784	16536		1.35	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3989	18737	28371	1.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4251	18992	28617	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	18992	28618	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	18992	28619	4.97	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5070	17780		2.39	8.2E-02	Z66893.1	NT	T.inflatum transposon Restless DNA
5252	18058	30687	1.49	8.2E-02	BE897030.1	EST_HUMAN	601439578F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	19661	32707	3.09	8.2E-02	AF306555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20298		0.57	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8670	21362	34509	2.95	8.2E-02	AW876126.1	EST_HUMAN	RC2-PT0004-031286-011-d05 PT0004 Homo sapiens cDNA
9499	22152	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9663	22315	35512	2.24	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355566 5'
12164	24646	31102	4.03	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12584	25138		3.65	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6688	18463	31378	0.79	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6286	19059	32040	1.19	8.1E-02	T11532.1	EST_HUMAN	A1484F Heer Homo sapiens cDNA clone A1484
7097	19786		0.66	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7482	20154		1.25	8.1E-02	AB926881.1	EST_HUMAN	wc86f08.x1 NC_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8238	20832	34067	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20832	34068	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9812	22463		1.64	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	15534	25447	5.03	8.0E-02	AW654653.1	EST_HUMAN	EST368723 MAGE resequences, MAGE Homo sapiens cDNA
915	13682	26344	0.78	8.0E-02	U60315.1	NT	Mollusca contagiosum virus subtype 1, complete genome
1694	15578	27134	9.85	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1694	15578	27135	9.85	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1898	14633	27343	3.27	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2374	15096	27835	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2374	15096	27836	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2473	15191		4.2	8.0E-02	BF246744.1	EST_HUMAN	801855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2823	13827	28486	0.98	8.0E-02	M23449.1	NT	Diatyocellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2801	15667	28315	1.45	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3797	16549	28182	1.01	8.0E-02	AW986118.1	EST_HUMAN	EST378191 MAGE resequences, MAGE Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4725	17457	30093	1.43	8.0E-02	AI434202.1	EST_HUMAN	i31g02x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2132114 3'
4764	17496		6.33	8.0E-02	X72794.1	NT	Mus musculus gene for galectinase B
5108	17828	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	UI-H-B1-att4-0-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547 3'
5801	18591	31516	3.15	8.0E-02	AF278948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18591	31516	1.82	8.0E-02	AF278948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9289	21956	35127	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9289	21956	35128	1.12	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10058	22706		0.55	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10892	23383	36623	2.27	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12195	24065	31070	6.39	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
12748	17903		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.9E-02	BE250008.1	EST_HUMAN	600943161F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856610 5'
2978	15744	28392	7.25	7.9E-02	AI682029.1	EST_HUMAN	ar68c08.x1 Baritised colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26875 60S RIBOSOMAL PROTEIN L38 (HUMAN);
3777	16529	29168	0.97	7.9E-02	AF030694.2	NT	Pleuroctidum falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG8 (cg8), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3832	16583	29217	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	16583	29218	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4845	17379	30011	0.98	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5'
4760	17492		1.31	7.9E-02	AB000919.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4851	17581	30204	1.02	7.9E-02	L24757.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
6597	19360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
7931	20628	33764	2.79	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
8627	22575	35773	4.21	7.9E-02	AI081044.1	EST_HUMAN	cu63505.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2 CE08811;
9627	22575	36774	4.21	7.9E-02	AI081044.1	EST_HUMAN	cu63505.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2 CE08811;
1188	13940	28604	1.77	7.9E-02	AI793275.1	EST_HUMAN	cc58c02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;
1188	13940	28605	1.77	7.9E-02	AI793275.1	EST_HUMAN	cc58c02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	16484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943056F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959893 5'
6076	19457	32479	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6076	19457	32480	0.88	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6084	21376	34520	0.71	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8779	21471	34616	0.66	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
8851	21842	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21842	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9281	22015	35183	1.07	7.8E-02	AA468354.1	EST_HUMAN	nc8808.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
9701	22352	35547	0.82	7.8E-02	Z99124.1	NT	Beclius subtilis complete genome (section 21 of 21); from 3989281 to 4214814
10562	23258	36494	4.58	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12764	26015		3.92	7.8E-02	AF098349.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1378	15588	26800	1.25	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	16326		1.97	7.7E-02	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5466	18256	31146	0.59	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33625	5.37	7.7E-02	AA402849.1	EST_HUMAN	zu53d11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
9735	22396	35590	3.94	7.7E-02	P38060	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10031	22879	35895	0.85	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
10031	22879	35896	0.85	7.7E-02	A1318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10933	23813	36893	4.51	7.7E-02	11422757	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
12389	25215		2.68	7.7E-02	11438659	NT	Homo sapiens KIA00828 gene product (KIA00828), mRNA
3382	16141	28798	1.97	7.6E-02	BE614432.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3403	16181	28812	1.14	7.6E-02	AA298447.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3547	16302	28962	0.71	7.6E-02	AJ400877.1	NT	EST112214 Cembellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6006	18787	31749	0.81	7.6E-02	A1061275.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
							an25g02.x1 Oesker Wilms tumor Homo sapiens cDNA clone IMAGE:1889730 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6263	19037	32012	0.92	7.6E-02	BE378328.1	EST_HUMAN	601238402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
9787	22448		1.63	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
10119	22767	35979	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-120800-017-c08 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE95938.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10487	23133	36359	0.71	7.6E-02	XG2858.1	NT	L. esculentum mRNA for trice phosphate translocator
10487	23133	36360	0.71	7.6E-02	XG2858.1	NT	L. esculentum mRNA for trice phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW990645.1	EST_HUMAN	QV3-BN0046-150400-151-c04 BN0046 Homo sapiens cDNA
767	13540	26199	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	26200	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	A1948714.1	EST_HUMAN	wq24h08.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2472257 3'
8296	20630	34066	1.05	7.5E-02	A1864357.1	EST_HUMAN	wf62b02.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8405	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
9932	22680		0.54	7.5E-02	BF221730.1	EST_HUMAN	7d61c05.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;
10360	23036	30252	0.7	7.5E-02	BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10488	23134	36361	0.72	7.5E-02	X79460.1	NT	C.fiml DSM 20113 16S rDNA
466	18260	25891	1.48	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA
1445	14192		0.92	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2585	15299		1.32	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3581	16336	28981	0.86	7.4E-02	A1807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4656	17390	30024	2.03	7.4E-02	L78810.1	NT	Homo sapiens ADPIA1TP carrier protein (ANT-2) gene, complete cds
4741	17473	30108	2.94	7.4E-02	6878442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
4889	17616	30235	2.1	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
6403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	y914g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7901	20495	33618	1.52	7.4E-02	BE680112.1	EST_HUMAN	601483360F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8399	21092	34228	1.03	7.4E-02	U50090.1	NT	Human periodic tyrophan protein 2 (PWFP2) gene, exons 15 to 21, and complete cds
9064	21753	34913	1.12	7.4E-02	AW629605.1	EST_HUMAN	h167d11.y1 NC1_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9084	21753	34914	1.12	7.4E-02	AW629605.1	EST_HUMAN	h167d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW_SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2:
9339	20410	33525	0.52	7.4E-02	A1872939.1	EST_HUMAN	wf74d02.x1 Soares_Dickgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2348819 3'
9339	20410	33526	0.52	7.4E-02	A1872939.1	EST_HUMAN	wf74d02.x1 Soares_Dickgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2348819 3'
9714	22365	35563	1.03	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
9841	22492	35692	0.52	7.4E-02	BF512878.1	EST_HUMAN	U1-H-BW1-ant-g-08-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
10939	23619	36869	1.28	7.4E-02	AA059167.1	EST_HUMAN	z84e01.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
12126	24618		1.53	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12381	25329		2.21	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-C81199-037-411 HT0243 Homo sapiens cDNA
486	13242	25881	1.5	7.3E-02	BE984961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
458	13242	25882	1.5	7.3E-02	BE984961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	13445	26085	3.9	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1484	15570	26900	3.62	7.3E-02	AW900281.1	EST_HUMAN	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1837	15580		12.41	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
6361	19131	32126	1.32	7.3E-02	AA779677.1	EST_HUMAN	z24e02.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7368	20048	33129	2.58	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8068	20782		1.15	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9110	21798		1.14	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11179	19131	32126	2.08	7.3E-02	AA779677.1	EST_HUMAN	z24e02.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
11844	24428		5.07	7.3E-02	11560138	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC84171), mRNA
117	12837	25577	1	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
117	12837	25578	1	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1458	14205	26890	2.72	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1458	14205	26891	2.72	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2852	15267		2.83	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3865	16815	29254	0.95	7.2E-02	AW298322.1	EST_HUMAN	U1-H-BW0-aj-e-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4312	17051	29676	4.85	7.2E-02	BF572307.1	EST_HUMAN	60207775F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4844	17378	30010	0.7	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome

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6205	18013	30635	2.88	7.2E-02	U87531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
6206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58	7.2E-02	BF218086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8087	20781	33910	0.8	7.2E-02	P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8902	21653		0.61	7.2E-02	Y17217.1	NT	Lactococcus lactis csfE gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22184	35346	2.32	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCA AUG01 5'
9859	22311	35509	3.8	7.2E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35867	0.93	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	h424f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q92340 Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
10082	22740	35955	0.62	7.2E-02	AA768204.1	EST_HUMAN	oa62c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10250	22898	36108	1.93	7.2E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	5.54	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685561 5'
10395	23041		3.68	7.2E-02	BE56214.1	EST_HUMAN	601068184F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10509	23155	36381	0.48	7.2E-02	AA706897.1	EST_HUMAN	z228h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10830	23512	36753	3.3	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Misl1 (Misl1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY006090.1	NT	Homo sapiens putative transmembrane protein decilin-1 mRNA, complete cds
12035	24580	31113	1.67	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:1048308 5'
12069	24593		4.45	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranaldi P) Homo sapiens cDNA clone PS13D5 3'
12182	24654		1.73	7.2E-02	U82828.1	NT	Homo sapiens elada telangiectasia (ATEM) gene, complete cds
12198	25185		8.19	7.2E-02	AW900982.1	EST_HUMAN	GM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12599	25362		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1897	14634	27344	2.01	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2280	15015	27751	5.07	7.1E-02	BF208902.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082981 5'
7807	20502	33622	0.77	7.1E-02	A125264.1	EST_HUMAN	qd82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1739922 3'

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11922	24483		6.41	7.1E-02	BE304764.1	EST_HUMAN	601149074F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13299	25831	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1488	14233		1.27	7.0E-02	X98677.1	NT	Martellia Mbuti-1 gene
1766	14498	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	z186104.s1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3027	15783	28440	2.1	7.0E-02	AW193152.1	EST_HUMAN	UI-H-B11-acy-c-07-Q-JL.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3878	16628	29268	0.74	7.0E-02	AA815438.1	EST_HUMAN	at5a12.s1 Scierus testis_NHT Homo sapiens cDNA clone 1375578 3' similar to gb:K03002 60S
4119	16961		1.28	7.0E-02	AW792862.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4189	16930	29560	1.06	7.0E-02	AF077821.1	NT	CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4877	17604	30227	7.24	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5293	18098		0.57	7.0E-02	Y08143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7300	19983	33059	1.29	7.0E-02	AV089285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7508	20177	33271	0.84	7.0E-02	Y19187.1	NT	AV689285 GK: Homo sapiens cDNA clone GKCAE06 5'
8998	21688	34838	1.26	7.0E-02	8628113	NT	Gallus gallus mRNA for partial accorin, XL spliced variant (acc gene)
9497	22150	35331	1.24	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
9852	22502	35702	0.51	7.0E-02	U27286.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11345	24035	37338	4.98	7.0E-02	AA724285.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	at99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507988	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	18625	29163	1.41	6.9E-02	Q08364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3773	18625	29164	1.41	6.9E-02	Q08364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (papC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glu-cole specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	601192383F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536253 5'
5127	17845	30462	1.25	6.9E-02	BE264805.1	EST_HUMAN	Canine distemper virus strain A7517, complete genome
7516	20187		0.61	6.9E-02	AF164967.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
7951	20646		1.12	6.9E-02	U12022.1	NT	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34282	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8451	21143	34283	1.01	6.9E-02	BE567435.1	EST_HUMAN	Barbale duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
9018	21708	34860	0.7	6.9E-02	U22967.1	NT	Xlaevis XFD2 mRNA for fork head protein
12065	24580		1.82	6.9E-02	X74315.1	NT	



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12232	24685		1.69	6.8E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG
12447	24817		1.46	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1875	14613	27321	1.56	6.8E-02	AA498759.1	EST_HUMAN	aa30f02r1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:887339 5' similar to gb:M22382
1875	14613	27322	1.58	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3097	15862	28503	1.19	6.8E-02	AA781986.1	EST_HUMAN	aa30f02r1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:887339 5' similar to gb:M22382
3097	15862	28504	1.19	6.8E-02	AA781986.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3097	15862	28505	1.19	6.8E-02	AA781986.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
4516	17251		0.86	6.8E-02	BE141076.1	EST_HUMAN	af75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
6525	19291		0.6	6.8E-02	P20792	SWISSPROT	af75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
6799	19480		1.09	6.8E-02	BE061860.1	EST_HUMAN	af75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
7180	19806	32869	8.73	6.8E-02	AL163288.2	NT	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7584	20252	33358	0.63	6.8E-02	U16886.1	NT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
8186	20890	34017	5.01	6.8E-02	AJ248287.1	NT	RC1-BT0264-010300-017-409 BT0264 Homo sapiens cDNA
8186	20890	34018	5.01	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C068
11873	25379		2.3	6.8E-02	T03214.1	EST_HUMAN	Dicystatium discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
12001	24537		2.86	6.8E-02	AA768014.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
12551	24898		1.65	6.8E-02	AW975839.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
12613	24920		3.06	6.8E-02	9010585	NT	FB4A8 Fetal brain, Strategene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
1519	14286		1.63	6.7E-02	AF115536.1	NT	af67f05.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
1886	14623	27333	2.27	6.7E-02	AJ220285.1	EST_HUMAN	EST387948 IMAGE:887339, MAGN Homo sapiens cDNA
3706	18459	28097	4.52	6.7E-02	P17278	SWISSPROT	Mus musculus titin TGF beta binding protein (Tgfb), mRNA
7749	20446	33567	0.65	6.7E-02	X62905.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1*01 allele, complete cds
7749	20446	33568	0.55	6.7E-02	X62905.1	NT	gg70a04.x1 Soares testis_NHT_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
8337	21030	34167	0.47	6.7E-02	AW082888.1	EST_HUMAN	HOMEOBOX PROTEIN HOXD-4 (HOXA-4)
9500	22153	35333	0.69	6.7E-02	AW137359.1	EST_HUMAN	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9500	22153	35334	0.86	6.7E-02	AW137359.1	EST_HUMAN	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
1348	14096	26771	1.07	6.6E-02	AF246116.1	NT	xb61c11.x1 Soares testis_NHT_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
2180	14909	27841	3.31	6.6E-02	AJ289241.1	NT	UI-HB1-ecr-g-01-QUL.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716433 3'
3456	16212	28805	10.57	6.6E-02	R04906.1	EST_HUMAN	UI-HB1-ecr-g-01-QUL.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716433 3'
3471	16227	28881	2.69	6.6E-02		NT	Drosophila melanogaster cactin mRNA, complete cds
3471	16227	28882	2.50	6.6E-02	7108357	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
					7108357	NT	Y18b10.s1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:138679 3'
						NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
						NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

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4060	16805	29436	1.29	6.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4921	17649	30261	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17649	30262	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6489	19258	32258	3.44	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6701	19283	32286	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20542	33670	1.81	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21065	34206	0.84	6.6E-02	AF060055.1	NT	Dicotyledonum discoidium darlin (darA) gene, complete cds
8678	21370		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8819	21511	34654	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8819	21511	34655	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9851	22501	35701	0.65	6.6E-02	AJ458752.1	EST_HUMAN	p97g06.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
9887	22635	36845	1.68	6.6E-02	Y07848.1	NT	Homo sapiens E2F5, gcr22, rrp22 and barn22 genes
10022	22670		0.63	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10883	23563	38811	6.88	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
11867	24461	37793	1.48	6.6E-02	AF062572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.66	6.6E-02	9837991	NT	Mus musculus D1PB gene (D1pb), mRNA
12740	25006		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	25977	2.49	6.6E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964178 5'
968	13732	26398	1.32	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26793	3.08	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27189	1.77	6.5E-02	AE000784.1	NT	Aquifex acidicus: section 98 of 109 of the complete genome
5471	18270	31162	2.03	6.5E-02	AA443991.1	EST_HUMAN	z46h12.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038
6877	17953	30549	0.95	6.5E-02	U22881.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
9842	22493	35693	0.55	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
9842	22493	35694	0.55	6.5E-02	BE963200.2	EST_HUMAN	601658817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	23010	36225	0.48	6.5E-02	BF106300.1	EST_HUMAN	601658817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10335	23232	36466	5.58	6.5E-02	AA195548.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11894	24463		3.73	6.5E-02	M21496.1	NT	z32g05.s1 Soares NIH-MP4_S1 Homo sapiens cDNA clone IMAGE:685144 3'
12240	24691		4.66	6.5E-02	AF102963.1	NT	Rabbit microsomal epoxide hydrolase
561	13343	25970	2.09	6.4E-02	X94549.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
3014	15780	28429	0.96	6.4E-02	6896923	NT	A. carterae precursor of peridinin-chlorophyll-protein (P-CP) gene
4839	15780	28429	1.18	6.4E-02	6896923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5363	18185	30850	1.67	6.4E-02	AI191956.1	EST_HUMAN	q07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;
5791	18582	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31763	4.21	6.4E-02	AF052733.1	NT	Heterodera glyxines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31764	4.21	6.4E-02	AF052733.1	NT	Heterodera glyxines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6308	19080	32065	0.62	6.4E-02	AI672898.1	EST_HUMAN	w73g12.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6719	19634	32677	5.43	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7360	20041	33119	0.64	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 617
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
8563	21255	34392	3.42	6.4E-02	AA033005.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21715	34868	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDA1A10
9486	22139		0.55	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
9617	22270	35457	1.73	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37629	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens nuclein 5B (MUC5B) gene, partial cds
12188	24659	31065	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF106905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; amRNp, G7A, NG23, MUs homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3590	16344		2.38	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6045	18825	31786	1.18	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087499 5'
7142	19829		0.82	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9191	21861	35028	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
9913	22662	35758	2.64	6.3E-02	AB010162.1	NT	Hepatitis G virus: RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10171	22819		0.85	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10615	19825	31786	2.98	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087499 5'
4224	18965	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 68

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4304	17043		1.02	0.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		0.31	0.2E-02	Q62181	SWISSPROT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6698	19615	32656	0.65	0.2E-02	D4630.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7527	20198	33292	1.03	0.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8846	25429		0.6	0.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35092	0.52	0.2E-02	AA78450.1	EST_HUMAN	af20a08.s1 Soares_t052_HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9390	22042	35214	1.65	0.2E-02	0677898	NT	Mus musculus striatal cell derived factor receptor 2 (Sdfr2), mRNA
11085	23765	37039	1.56	0.2E-02	AF217490.1	NT	Homo sapiens fragile 100 oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	0.2E-02	AJ242735.1	NT	Melanizidum antisense mRNA for Chymotrypsin (chy1 gene)
11865	24449	37791	1.74	0.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoyltransferase precursor (Ugpf) mRNA, complete cds
11989	25405		13.39	0.2E-02	AE000750.1	NT	Aquifex aeolicus: section 82 of 109 of the complete genome
12394	24782	31037	2.5	0.2E-02	BF112039.1	EST_HUMAN	737h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q8Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
249	13058	25697	5.59	0.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3972	16721		2.29	0.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKCT1) gene, complete cds
6023	18803		1.4	0.1E-02	4507070	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33986	3.75	0.1E-02	X90288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8559	21251	34388	0.57	0.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
8559	21251	34389	0.57	0.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
10630	23323	36560	4.91	0.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-138-C06 HT0818 Homo sapiens cDNA
11862	24446	37787	1.27	0.1E-02	AB025333.1	NT	Epitetrax burgeri mRNA for RNA polymerase III largest subunit, partial cds
11945	25323		2.27	0.1E-02	X70989.1	NT	S. japonicum mRNA for serine-enzyme
12633	24633		5.61	0.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
96	12922	25559	0.76	0.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
96	12922	25560	0.76	0.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
1239	13988	26655	1.54	0.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 135 of the complete genome
2682	15391	28130	1.09	0.0E-02	AW968846.1	EST_HUMAN	EST380924 MA3E resequencing, MAGJ Homo sapiens cDNA
2775	15480		1.62	0.0E-02	AB031289.1	NT	Mesocricetus cord mitochondria DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2937	12922	25559	0.9	0.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2937	12922	25560	0.9	0.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	15986	28639	1.48	6.0E-02	AA372378.1	EST_HUMAN	EST84286 Cdxn adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15986	28640	1.48	6.0E-02	AA372378.1	EST_HUMAN	EST84286 Cdxn adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE064443.2	EST_HUMAN	601658150R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3876060 3'
5037	17758	30370	0.69	6.0E-02	AF146738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011189-013-b04 BT0253 Homo sapiens cDNA
6122	18900	31868					wf48h05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains
6891	17907	30524	0.77	6.0E-02	AI607537.1	EST_HUMAN	L1.1 L1 L1 repetitive element;
6891	17907	30524	3.07	6.0E-02	5174098	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
6891	17907	30525	3.07	6.0E-02	5174098	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7088	19777	32842	2.33	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7580	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf58h08.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1764199 3'
8321	21014		0.54	6.0E-02	11468496	NT	Recitomonas americana mitochondrion, complete genome
9172	21842	35007	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78h06.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	35008	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78h06.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9306	21973	35147	1.66	6.0E-02	AI245365.1	NT	Acipenser baeri partial IGL V gene for immunoglobulin light chain variable region, exons 1-2
9306	21973	35148	1.66	6.0E-02	AI245365.1	NT	Acipenser baeri partial IGL V gene for immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11306	23965		1.69	6.0E-02	AA126386.1	EST_HUMAN	zn87c08.t1 Strabagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31084	2.19	6.0E-02	11431702	NT	Homo sapiens cDNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12584	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf68h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358885 3' similar to TR:O60298
223	13035	26671	3.87	5.9E-02	AW664719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN ;
2882	15748	28396	2.89	5.9E-02	AF190289.1	NT	RC1-DT0001-20100-012-010 DT0001 Homo sapiens cDNA
4817	17548	30173	1	5.9E-02	AF006304.1	NT	Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
5123	17841	30457	0.73	5.9E-02	AW028748.1	EST_HUMAN	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17841	30458	0.73	5.9E-02	AW028748.1	EST_HUMAN	wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
8515	21207	34350	1.88	5.9E-02	9055249	NT	O65386 F12F1.20 PROTEIN ;
9351	20422		0.8	5.9E-02	BF242748.1	EST_HUMAN	wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
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							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
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							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
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							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
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							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
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							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;
							Mus musculus f53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
							Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
							wf34h02.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN ;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23378		3.2	5.9E-02	6679870	NT	Mus musculus iclialath-like (Fet), mRNA
10944	23023	36872	1.44	5.9E-02	11433356	NT	Homo sapiens rhelin (LOC51198), mRNA
11544	24144		1.50	5.8E-02	A1240733.1	NT	Gallus gallus HICQ telomere junction
912	13679		5.18	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2864	15632		0.96	5.8E-02	A1223621.1	NT	Populus trichocarpa GCoADMT1 gene, exon 1 to exon 5
4322	17061	29687	4.9	5.8E-02	AW061927.1	EST_HUMAN	wx24-02.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17061	29698	4.9	5.8E-02	AW061927.1	EST_HUMAN	wx24-02.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	A1247505.1	EST_HUMAN	qh5801.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4510	17245	29880	4.95	5.8E-02	A1247505.1	EST_HUMAN	qh5801.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF068284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33362	2.90	5.8E-02	M69150.1	NT	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	M69150.1	NT	Human polymorphic microsatellite DNA
8565	21257	34394	0.87	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12084	24500		1.79	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25398		7.08	5.8E-02	AA604269.1	EST_HUMAN	no76e11.at NCI_CGAP_AA11 Homo sapiens cDNA clone IMAGE:1112684 3'
3053	15819	28463	1.36	6.7E-02	A081644.1	EST_HUMAN	ou63b05.at NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3068	15834	28478	1.29	5.7E-02	AF119117.1	NT	CE086111;
						NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3694	16448		0.97	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3783	16535	29173	2.45	5.7E-02	AW966791.1	EST_HUMAN	EST378865 MAG3E resequences, MAG1 Homo sapiens cDNA
4637	17371		1.01	5.7E-02	M95096.1	NT	Boe taurus lysoczyme gene (cow 3), complete cds
7438	20115	33203	0.89	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7438	20115	33204	0.89	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
9055	20749	33980	1.42	5.7E-02	A1296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
9760	22401	35606	0.84	5.7E-02	6681260	NT	Mus musculus e-12 oncogene (Ect2), mRNA
11143	23810	37090	4.42	5.7E-02	A1762995.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11143	23810	37091	4.42	5.7E-02	A1762995.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11321	24012		1.59	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12285	26213		7.24	5.7E-02	D50320.1	NT	Pig DNA for SPA-2, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12515	25283		3.18	5.7E-02	AF217490.1	NT	Homo sapiens fragile 160 oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	AF261280.1	NT	Paratuberculosis apolipoprotein-E gene, complete cds
1518	14285	28951	1.57	5.8E-02	AF084455.1	NT	Hydroxycyloleulin ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4595	17330	28957	1.12	5.8E-02	AB013100.1	NT	Lycopodium obscurum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4848	17382	30014	1.46	5.8E-02	AA280599.1	EST_HUMAN	z445c01.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6562	19327	32334	6.57	5.8E-02	AW172708.1	EST_HUMAN	x02a10.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:084979 O84979 KIAA0805 PROTEIN.
8791	19535	32563	1.25	5.8E-02	AA866182.1	EST_HUMAN	cd47712.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7051	19742	32804	3.05	5.8E-02	BE008001.1	EST_HUMAN	QV0-BN0147-230400-214-g07 BN0147 Homo sapiens cDNA
7063	19764	32819	0.69	5.8E-02	AB983738.1	EST_HUMAN	w234705.x1 NC1_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2550689 3' similar to gb:X06408 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20388	33502	0.66	5.8E-02	AI183583.1	EST_HUMAN	q064g11.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1734306 3'
8701	21363	34539	2.88	5.8E-02	BE542863.1	EST_HUMAN	80108718F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8701	21363	34540	2.88	5.8E-02	BE542863.1	EST_HUMAN	80108718F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9712	22363	35561	1.09	5.8E-02	AA482864.1	EST_HUMAN	nf48d07.s1 NC1_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.
11556	24155		2.35	5.8E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2690	15370	28108	6.8	5.5E-02	X97899.1	NT	H.sapiens gene encoding La autoantigen
3209	15972	28625	3.93	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4191	16932	29561	1	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5635	18370	31281	3.58	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038	2	5.5E-02	8755902	NT	Mus musculus tufellin 1 (Tuf1), mRNA
8019	20714	33845	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8019	20714	33846	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9555	22208	35392	0.6	5.5E-02	10947034	NT	Homo sapiens ei F4E-transporter (4E-T), mRNA
9555	22208	35393	0.6	5.5E-02	10947034	NT	Homo sapiens ei F4E-transporter (4E-T), mRNA
9650	22302	35497	1.32	5.5E-02	U09492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10943	23622	36871	7.28	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cia) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhaf), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB).>



Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12797	25349	30604	1.49	5.6E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3019	15785		0.91	5.4E-02	AJ277468.1	NT	Oryza sativa rib33-1 gene for putative Bowman Birk trypsin inhibitor
3416	17885		5.78	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-1 40200-012-C03 BT0559 Homo sapiens cDNA
3891	16641	29281	0.76	5.4E-02	U65806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395261 to 2613730
8969	21659	34809	0.55	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	36467	1.62	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01	5.4E-02	U20790.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37076	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-1 90700-021-D06 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-1 90700-021-D06 FN0112 Homo sapiens cDNA
1031	13791	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-0.21298-062-e08 ST0213 Homo sapiens cDNA
1031	13791	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-0.21298-062-e09 ST0213 Homo sapiens cDNA
1495	14242	26929	14.72	5.3E-02	T94759.1	EST_HUMAN	ye07f12.1 Strain gene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2501	15218	27961	2.47	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2943	15709	28360	0.95	5.3E-02	M59417.1	NT	Pseudomonas putida ttpS gene
2943	15709	28361	0.95	5.3E-02	M59417.1	NT	Drosophila melanogaster leminin B2 gene, complete cds
3150	15913	28558	5.51	5.3E-02	AJ276408.1	NT	Drosophila melanogaster leminin B2 gene, complete cds
5028	17749	30361	6.34	5.3E-02	M80463.1	NT	Pseudomonas putida ttpS gene
5236	18042	30670	1.98	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5236	18042	30671	1.98	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785	19529	32556	5.01	5.3E-02	9695413	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6992	19685	32733	1	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7280	19944		2.06	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7777	20399	33514	0.65	5.3E-02	P38742	SWISSPROT	nuclear protein 11F1 isoform [mice, mRNA, 4053 nt]
8304	20996		0.7	5.3E-02	U10096.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
9023	21713	34867	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
10032	22680	35897	0.62	5.3E-02	AB022805.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10032	22680	35898	0.62	5.3E-02	AB022805.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
							Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10156	22804		0.63	5.3E-02	Y07907.1	NT	D. rerio mRNA for xp-23 POU gene, splice variant (neurula, 9-16 hpf and posttranscription, 20-28 hpf)
10230	22878	36090	0.7	5.3E-02	X58432.1	NT	B. rerio pou(c) mRNA for transcription factor



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12776	25030	30864	1.43	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		180.56	5.2E-02	5031908	NT	Homo sapiens neprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3112	15877	28516	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	15877	28517	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16869	29310	1.23	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Ord1) mRNA, complete cds
3921	16871		1.19	5.2E-02	6671757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4245	16986	29609	3.02	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nkr-1 mRNA, complete cds
5053	17772		0.9	5.2E-02	AA297940.1	EST_HUMAN	EST11352 Uterus Homo sapiens cDNA 5' and
5828	18617	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdb54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AJ830665.1	EST_HUMAN	W90604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element:
7174	19880	32932	3.13	5.2E-02	P38322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8095	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9628	22282	35472	1.87	5.2E-02	D10827.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9629	22282	35473	1.87	5.2E-02	D10827.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24795		1.93	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2364	15088		1.17	6.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D073 5'
4179	16819	29547	1.03	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4980	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6575	16339	32360	0.72	6.1E-02	AF280369.1	NT	HIV-1 patient 04 from Italy protease (pol) gene, complete cds
6780	17929	30564	1.44	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8151	20845	33975	0.84	5.1E-02	M20434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPR1) gene, complete cds
8151	20845	33976	0.84	5.1E-02	M20434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPR1) gene, complete cds
8245	20939	34076	1.48	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
8783	21475	34622	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8783	21475	34623	0.58	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9709	22360	35556	6.2	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.89	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN GEX)
10733	23420	36861	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	36862	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
12421	24797		2.56	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12679	24968		1.41	5.1E-02	AA534104.1	EST_HUMAN	h73f02.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:988139
470	13256	25894	1.84	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13934	26569	6.54	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1983	14719	27438	3.91	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	26397	1.28	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (ULK2), mRNA
3562	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3672	16425	28096	5.83	5.0E-02	U12789.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4770	17502		0.99	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18819	31780	0.95	5.0E-02	AF098284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7437	20114	33202	12.48	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10100	22748	35963	1.28	5.0E-02	AF308238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10821	23167		0.45	5.0E-02	BF213260.1	EST_HUMAN	801844763F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E-02	U67800.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11956	25249		3.5	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13168	25800	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13168	25801	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	16043	28692	2.53	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3556	16311		0.89	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632826 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3579	16334	28978	0.99	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3579	16334	28979	0.99	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	17519	30142	1.91	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
5286	18091	30751	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7042	19733	32783	0.91	4.9E-02	AEO00980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AE0002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8552	21344	34489	0.71	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191	22839	36054	0.48	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36396	0.46	4.9E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23986	37285	3.22	4.8E-02	AF08303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12345	24752		1.77	4.8E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12598	24912		3.41	4.8E-02	M18964.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
476	13262	25899	9.96	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14997	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3203	15066	28620	2.1	4.8E-02	X17144.1	NT	Tetrahymena tetrahymena histone H3II and histone H4II intergenic DNA
4623	17358		1.15	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5144	17863	30478	1.03	4.8E-02	11893131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
5144	17863	30479	1.03	4.8E-02	11893131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33864	1.32	4.8E-02	AW388497.1	EST_HUMAN	MF2-ST0129-221099-012-b02 ST0128 Homo sapiens cDNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
6731	19595	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	yz87f09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
6819	19480	32503	2.02	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-39-DNA-binding protein
8852	21543	34690	0.98	4.7E-02	X98211.1	NT	H. sapiens DNA for endogenous retroviral like element
8875	21566		2.68	4.7E-02	AB028878.1	NT	Gallus gallus Wpkci-8 gene, complete cds
9127	21815	34981	6.89	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-39-DNA-binding protein
9547	22200	35382	0.67	4.7E-02	BF306237.1	EST_HUMAN	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9635	22287		0.57	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10854	23345	36582	1.4	4.7E-02	8754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11545	24145	37453	1.39	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11545	24145	37454	1.39	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
264	13072	25712	0.93	4.6E-02	BE163883.1	EST_HUMAN	PMO-HT0330-261199-003-g05 HT0339 Homo sapiens cDNA
722	13496	26149	2.91	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1269	14018		0.99	4.6E-02	A014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1338	14088	26762	3.47	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element LTR1 repetitive element;
							AV727059 HTC Homo sapiens cDNA clone HTCBCW01 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2492	15209	27951	2.31	4.6E-02	AW230023.1	EST_HUMAN	xm24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2894653 3' similar to SW:GRF1_HUMAN
2811	13072	25712	1.9	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
3325	15774	28423	0.74	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3487	15774	28423	0.73	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g06 HT0339 Homo sapiens cDNA
4103	16946		1.35	4.6E-02	AF220365.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							Mus musculus nuclear RNA helicase II/Gu (dbx21) gene, complete cds
5121	17839	30455	0.99	4.6E-02	AA079157.1	EST_HUMAN	zm92c10.s1 Strategene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
							Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
5647	18442	31365	1.57	4.6E-02	AF076902.1	NT	C.reinhardtii atp2 (atpB) mRNA
6136	18914	31883	3.51	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6136	18914	31884	3.51	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6702	19817	32859	1.47	4.6E-02	A146574.1	EST_HUMAN	q60b06.x1 Soares_placenta_86c6weeks_2Nb1P8b59W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element;
8554	21246	34386	2.69	4.6E-02	BE154006.1	EST_HUMAN	PM0-HT0339-00400-009-G12 HT0339 Homo sapiens cDNA
11379	23986	37286	4.94	4.6E-02	AA913328.1	EST_HUMAN	cd27f09.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12325	24744		1.88	4.6E-02	AV712871.1	EST_HUMAN	AV712871 DCA Homo sapiens cDNA clone DCAAZF07 5'
12705	24985		3.98	4.6E-02	X37808.1	NT	Human germ-line immunoglobulin lambda light chain gene
434	13220	25868	1.72	4.6E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1198	13948	28612	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1198	13948	28613	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2103	14834	27568	3.76	4.5E-02	AE003984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3710	18463	28102	3.66	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6137	18915	31885	1.61	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C080
6415	19163	32182	0.77	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6779	19523	32550	0.61	4.5E-02	L26487.1	NT	Methanococcus frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
6779	19523	32551	0.61	4.5E-02	L26487.1	NT	Methanococcus frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8292	20888	34125	1.98	4.5E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
9849	22499	35688	4.57	4.5E-02	AA325216.1	EST_HUMAN	EST28187 Cerebellum II Homo sapiens cDNA 5' and similar to similar to neuro-D4 protein
10000	22648	35860	0.48	4.5E-02	X95808.1	NT	A.europaeum mRNA for legumin-like protein

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10116	22764	35976	0.85	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12154	24640	31097	1.94	4.5E-02	11418013	NT	Homo sapiens rat finger protein-like 3 (RPPL3), mRNA
12537	25290	30733	6.91	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	13025		5.52	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2089	14821		5.42	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2494	15211	27953	2.4	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-110300-070-g02 PT0012 Homo sapiens cDNA
3631	16384	29024	1.95	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4584	17319	29945	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4584	17319	29946	1.24	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4693	17427		2.28	4.4E-02	AJ222689.1	NT	Ovis aries GCAAT-enhancer binding protein epsilon gene
7018	19710	32768	0.64	4.4E-02	AF066824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7018	19710	32767	0.64	4.4E-02	AF066824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8650	21342	34486	2.14	4.4E-02	AA736969.1	EST_HUMAN	nv13h03.s1 NC1_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11007	23679	36938	2.62	4.4E-02	AF060699.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11157	23824	37104	2.78	4.4E-02	AA498739.1	EST_HUMAN	ae33f04.r1 Gesler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
11890	24460		2.57	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12087	25408		1.87	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4107418 5'
763	13536	26195	7.07	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2573	15287	28024	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADEI Homo sapiens cDNA clone ADBA0H08 5'
3423	16180	28630	7.84	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3651	16404		1.37	4.3E-02	AF060698.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5162	17869	30482	0.95	4.3E-02	U11768.1	NT	Grapevine fanleaf virus coat protein gene, partial cds
6404	19173	32171	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6404	19173	32172	4.3	4.3E-02	P30427	SWISSPROT	PLECTIN
6633	19395	32410	0.73	4.3E-02	AA652266.1	EST_HUMAN	ns06c12.s1 NC1_CGAP_P72 Homo sapiens cDNA clone IMAGE:1188886
8411	21104	34243	0.73	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8700	21392	34537	1.02	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8700	21392	34538	1.02	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
803	15676	26238	2.7	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
846	13616		2.32	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
876	13945	26315	1.35	4.2E-02	AW003045.1	EST_HUMAN	w34g01.x1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:264584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 mRNA, contains L1.3 L1 repetitive element;
1714	14457		1.02	4.2E-02	AL445086.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1771	14513	27213	1.01	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3655	16408	29047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	29471	0.7	4.2E-02	BE262605.1	EST_HUMAN	601150933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	29648	1.83	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4284	17023	29649	1.83	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4695	17429	30060	2.32	4.2E-02	BF342995.1	EST_HUMAN	602017105F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4152672 5'
5530	18328	31231	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5530	18328	31232	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6886	17962	30517	0.56	4.2E-02	BE268285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2988319 5'
7426	20103	33190	4.7	4.2E-02	AF276762.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8710	21402	34547	3.96	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10084	22712	35930	1.22	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-66)
10989	23845	36898	2.82	4.2E-02	AA976118.1	EST_HUMAN	on33b11.a1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568461 3' similar to gb:M65290
11278	23939	37231	2.54	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11278	23939	37232	2.64	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11489	24090	37402	1.68	4.2E-02	AF176458.1	NT	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12415	25335		3.43	4.2E-02	AJ983494.1	EST_HUMAN	PRRS isolate PRRSV38 envelope glycoprotein gene, complete cds
497	13281	26916	1.24	4.1E-02	AF200628.1	NT	w48g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2683	15392	28131	1.04	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4439	17175		7.52	4.1E-02	AW893484.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5556	18353	31262	0.82	4.1E-02	BE251894.1	EST_HUMAN	QV1-NN0012-180400-164-008 NN0012 Homo sapiens cDNA
5556	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6783	19527		0.67	4.1E-02	X75881.1	NT	601107536F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6889	19891	32742	1.25	4.1E-02	AE002132.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7413	20090	33174	2.09	4.1E-02	7662347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
							Homo sapiens KIAA0887 protein (KIAA0887), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33285	0.68	4.1E-02	L02110.1	NT	Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitose-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8541	21233	34376	0.68	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9052	21741	34899	0.81	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Coken adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25338	30715	4.07	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3238	19000	29650	3.26	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5295	18100	30759	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18898	31866	0.93	4.0E-02	BF110434.1	EST_HUMAN	7n62h07.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568390 3' similar to TR:O75296 O75296 R29124_1.
7590	20258	33368	6.57	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7666	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	21309	34451	2.22	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S162 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	BF979378.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9567	22220	35408	4.01	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, ThdH:formate reductase subunit A
9854	22534		1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24369		1.54	4.0E-02	AJ001018.1	NT	Kluweromyces fragilis gene for Car+ ATPase
12053	25158	30898	3.31	4.0E-02	AJ001058.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1096	13856	26516	2.75	3.9E-02	BF516149.1	EST_HUMAN	UIH-BW1-exon1-08-OJL.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1964	14689	27402	2.4	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2708	15415		1.69	3.9E-02		NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118	16880	29487	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16880	29488	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913	0.55	3.9E-02	D50808.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.9E-02	D50808.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5644	18439	31353	1.04	3.9E-02	BE98841.1	EST_HUMAN	601640874F1 NIH_MGC 74 Homo sapiens cDNA clone IMAGE:3933642 5'
5766	18557	31484	0.95	3.9E-02	BF675203.1	EST_HUMAN	602136132F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4274910 5'
6857	19439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435	33557	1.14	3.9E-02	BF236813.1	EST_HUMAN	601808848F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134779 5'
7959	20654	33778	0.79	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20654	33779	0.79	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11386	20396	33511	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25298		15.98	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24883		1.83	3.9E-02	U60061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12666	25223		5.31	3.9E-02	AL049896.2	NT	Mus musculus chromosome X contig8; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mimm28orf
1945	14880	27394	1.16	3.8E-02	BE886137.1	EST_HUMAN	601510891F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.8E-02	AJ251973.1	NT	Homo sapiens partial steatrh-1 gene
4876	17603	30226	1.1	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2FM2 Homo sapiens cDNA clone NT2RM2001698 5'
5354	18157	30840	1	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
5996	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7218	19903	32976	1.66	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 8 (ABCA8), mRNA
8562	21254		1.33	3.8E-02	M00675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10549	23245	36481	2.62	3.8E-02	AF143952.2	NT	Homo sapiens PLEOTA (PELOTA) gene, complete cds
971	13736	28401	4.94	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1367	14115	26780	0.91	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2230	14958	27698	3.84	3.7E-02	A084808.1	EST_HUMAN	wf65608x1 NCJ CGAP Kbt11 Homo sapiens cDNA clone IMAGE:2404502 3'
2582	15296	28034	0.92	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	15911	28457	0.9	3.7E-02	P79644	SWISSPROT	ECMESODERMIN
3047	15913	28458	2.99	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203		1.17	3.7E-02	6680541	NT	Mus musculus pectussum large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
6976	25422		0.83	3.7E-02	AP0000083.1	NT	Aeropyrum pernix genomic DNA, section 8/7



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7592	20280	33368	0.58	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 220 of the complete genome
9914	22563		1	3.7E-02	AA782516.1	EST_HUMAN	af55c09.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1360912 3'
11864	24506	37811	3.86	3.7E-02	BF124974.1	EST_HUMAN	601792177F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12803	25193	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3646	16398	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3854	16407	29046	0.88	3.6E-02	AL088808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5341	18144	30806	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30921	0.84	3.6E-02	AF181722.1	NT	Homo sapiens FIU2AS (RU2) mRNA, complete cds
6807	19370	32382	6.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6807	19370	32383	5.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6885	19878	32725	2.5	3.6E-02	AF025852.1	NT	Chromatium vibrio sulfur globule protein C/2 precursor (sgp2) gene, complete cds
7206	19891	32867	2.78	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_me2
7533	20203	33298	1.03	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9291	21858	35130	1.72	3.6E-02	U20608.1	NT	MRO-HT0158-Q10200-003-b08 HT0158 Homo sapiens cDNA
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22165	35347	0.83	3.6E-02	BF347586.1	EST_HUMAN	602020453F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4166116 5'
11135	23803	37080	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11135	23803	37081	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11862	24436		1.46	3.6E-02	AL280966.1	EST_HUMAN	qk48p09.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1872185 3'
875	13644	26314	1.08	3.5E-02	U06506.1	NT	Drosophila melanogaster 10gtrh mRNA, complete cds
988	13751	26413	1.39	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1556	14303	26891	1.55	3.5E-02	BF878085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377 5'
1556	14303	26892	1.55	3.5E-02	BF878085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377 5'
4188	16929	29559	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 130 of the complete genome
4281	17020	29647	1.27	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6127	18905	31873	1.77	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20372		0.78	3.5E-02	H28851.1	EST_HUMAN	yp44a05.r1 Sources retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element
8521	21213	34357		3.5E-02	BE988970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
9917	22566	35762	1.45	3.5E-02	X78642.1	NT	L.lactis MG1363 grpE and dnaK genes
9965	22613	35817	0.5	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11477	24078	37388	1.82	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0328-291299-002-h03 CT0328 Homo sapiens cDNA
11477	24078	37389	1.82	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0328-291299-002-h03 CT0328 Homo sapiens cDNA
12596	25234		5.69	3.5E-02	BE276948.1	EST_HUMAN	601176765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13789	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	ix28407.x1 Sources NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:G211_HUMAN PS3801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1184	13636		7.14	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2391	15112	27849	2.06	3.4E-02	T57160.1	EST_HUMAN	yp20e06.r1 Stratiene lung (#637210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3424	16181	28831	1.4	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	16509	29145	0.7	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-010700-011-410 FN0155 Homo sapiens cDNA
3900	16650	29291	3.19	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0016-210200-021-A10 UM0016 Homo sapiens cDNA
4559	17294	29822	2.41	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
5000	17723		3.59	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5019	17740	30349	1.2	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6754	17923	30558	4.73	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8159	20853		3.25	3.4E-02	A1886629.1	EST_HUMAN	w89404.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2433031 3'
8646	21338	34482	1.36	3.4E-02	AA864986.1	EST_HUMAN	nu7008.s1 NCI_CGAP_Alt1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Stratiene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
8814	21506		5.97	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDGVLKATMRFNTEITAENL.TINLKESVTADAGRVEITAANSSGTTKAFINNVLDPRG
9678	22330		0.63	3.4E-02	A062719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGSQVNTYLLKRETSATVTEVSATVARTMMKVMKL ... ;
363	13161		9.61	3.3E-02	AA398735.1	EST_HUMAN	oz98r08.x1 Sources parathyroid_tumor_NbH4PA Homo sapiens cDNA clone IMAGE:1883519 3'
1143	13898	26559	17.86	3.3E-02	AB035867.1	NT	z75e06.s1 Sources testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
							Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14238	28923	1.16	3.3E-02	L16870.1	NT	Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3
1635	14381	27088	1.47	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.29	3.3E-02	AE000700.1	NT	Aquifex acidicus section 32 of 109 of the complete genome
2077	14909		2.46	3.3E-02	R09112.1	EST_HUMAN	Y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27910	1.31	3.3E-02	8755862	NT	Mus musculus tumor rejection antigen gp98 (Tra1), mRNA
4156	14381	27088	2.44	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4435	17171	28900	1.78	3.3E-02	8755862	NT	Mus musculus tumor rejection antigen gp98 (Tra1), mRNA
6336	19108	32095	27.36	3.3E-02	BF245965.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19108	32096	27.36	3.3E-02	BF245965.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20085	33180	0.63	3.3E-02	AF124162.1	NT	Nicotiana plumbaginifolia methylglutathione synthase sulphurylase (mtS) gene, partial cds
9222	21901	35071	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21901	35072	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35182	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.a1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9324	21901	35183	0.66	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11065	23735	37008	3.63	3.3E-02	BF691107.1	EST_HUMAN	ad08f09.a1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
12142	24630		3.24	3.3E-02	T96545.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12259	24704		1.52	3.3E-02	AF289665.1	NT	602247171F1 NH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 6'
12288	24718		2.92	3.3E-02	M81890.1	NT	ye49f11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
129	12944	25588	0.74	3.2E-02	AJ02005.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
1104	13881	26520	7.01	3.2E-02	AF096275.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1104	13881	26521	7.01	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
2112	14843		3.01	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 83 (hsp83) gene, hsp83d allele, complete cds
3131	15898	28540	10.06	3.2E-02	BE867353.1	EST_HUMAN	Drosophila melanogaster heat shock protein 83 (hsp83) gene, hsp83d allele, complete cds
3701	18454	29094	0.92	3.2E-02	AL163203.2	NT	LARGE TEGUMENT PROTEIN
3942	18692	29330	1.84	3.2E-02	Z74103.1	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3942	18692	29331	1.84	3.2E-02	Z74103.1	NT	Homo sapiens chromosome 21 segment HS21C003
4163	16234		14.21	3.2E-02	X94768.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL055c
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL055c
4894	17621		1.08	3.2E-02	AF108906.1	NT	H. sapiens RP3 gene (XLRP gene 3)
5448	18247	31135	1.83	3.2E-02	X68709.1	NT	Sedfraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
							Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G8A, NG22, G9, HSP70, HSC70t, end antRNP genes, complete cds; GTA gene, partial cds; and unknown genes
							S. griseocarneum whiG-Stv gene

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18247	31136	1.83	3.2E-02	X68709.1	NT	S.griseocaudum whiG-Stv gene
6431	19189	32198	3.13	3.2E-02	M32437.1	NT	Rat/polyoma virus: left junction in cell line W98.14
6432	19200		33.46	3.2E-02	T89367.1	EST_HUMAN	yc33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element;
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
7662	20328	33436	0.84	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8189	20863	34030	4.84	3.2E-02	6880565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
8839	21531		0.73	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9125	21813	34978	1.21	3.2E-02	A1279871.1	EST_HUMAN	qm17b04.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9125	21813	34979	1.21	3.2E-02	A1279871.1	EST_HUMAN	qm17b04.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9957	22805		4.07	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares pineal_gland_N3H-PG Homo sapiens cDNA clone IMAGE:397151 3' similar to gbL08441 CYTICHRONE C OXIDASE POLYPEPTIDE III (HUMAN);
10256	22804	36114	0.95	3.2E-02	U98762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	13989		2.14	3.1E-02	4503418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1282	14032	26702	1.72	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14622	27332	1.09	3.1E-02	9671564	NT	Mus musculus acetylcholine receptor protein complex AP-3, delta subunit (Ap3d), mRNA
1967	14703		1.34	3.1E-02	Z50087.1	NT	Drosophila melanogaster mRNA for headcase protein
5182	17890	30509	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5278	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5591	18398	31288	0.74	3.1E-02	BF887742.1	EST_HUMAN	602066783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4066789 5'
5828	25072	31338	0.59	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, strain FAM18
8940	21532	34677	0.46	3.1E-02	BE865022.2	EST_HUMAN	601658878R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3880281 3'
9931	22579	35778	2.93	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
11795	24396	37696	1.78	3.1E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
1619	14366		1.98	3.0E-02	AF187125.1	NT	Pityokine minus cytochrome c oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2590	15304	28040	0.97	3.0E-02	AA402242.1	EST_HUMAN	z65h103.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3645	18398	28038	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	18480		0.74	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150-040-e08 ST0286 Homo sapiens cDNA
3929	18679		1.42	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal_gland II Homo sapiens cDNA 5' and
4991	17714	30318	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6160	18937	31805	1.4	3.0E-02	N89615.1	EST_HUMAN	z339a10.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6160	18937	31806	1.4	3.0E-02	N89615.1	EST_HUMAN	z339a10.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6892	19609	32948	3.32	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)
6808	19467	32488	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6808	19467	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6971	19453	32472	2.15	3.0E-02	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6971	19453	32473	2.15	3.0E-02	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19819	32885	1.4	3.0E-02	M86524.1	NT	Human dydrophilin gene
7483	20155		0.59	3.0E-02	BF246381.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720		0.48	3.0E-02	BF079706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285654 5'
8639	21231	34373	0.66	3.0E-02	BF353898.1	EST_HUMAN	IL5-HIT0704-28000-108-c04 HIT0704 Homo sapiens cDNA
8892	21384		1.8	3.0E-02	AF275654.1	NT	Ornithomycinus anatinus coagulation factor X mRNA, complete cds
10357	23004	36221	1.49	3.0E-02	AE001797.1	NT	Thermoboga maritima section 109 of 138 of the complete genome
10446	23062	36322	0.49	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23862	37148	2.73	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12243	26389	30618	2	3.0E-02	R32019.1	EST_HUMAN	Y63d04.s1 Sources placenta Nb21P Homo sapiens cDNA clone IMAGE:134407 3'
12587	24909		2.46	3.0E-02	AW895565.1	EST_HUMAN	QV4-NIN0038-270400-187-H05 NIN0038 Homo sapiens cDNA
12629	25383		2.06	3.0E-02	AF048887.1	NT	Rattus norvegicus: UDP-Gal:glucosyltransferase beta-1,4-galactosyltransferase mRNA, complete cds
2436	16894	27891	1.27	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2890	15758	28402	1.04	2.9E-02	BE665844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
2990	15756	28403	1.04	2.9E-02	BE665844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3008	16658	28290	0.89	2.9E-02	H72805.1	EST_HUMAN	yu07e10.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18754	31715	0.97	2.9E-02	AF060221.1	NT	Sus scrofa decarboxylase II mRNA, complete cds
6189	18675	31853	7.39	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855598 5'
6855	19555	32585	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flhC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32904	12.03	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7987	20592	33723	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7987	20592	33724	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9558	22211	35396	2.49	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9558	22211	35397	2.49	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9774	22425		0.75	2.9E-02	AW876597.1	EST_HUMAN	EST1388708 MAGe sequences, MAGN Homo sapiens cDNA
10243	22891	36103	1.25	2.9E-02	AP000004.1	NT	Aeropyrum pernix genomic DNA, section 777
10977	17902	30590	1.97	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
552	13335		0.96	2.9E-02	AW970153.1	EST_HUMAN	EST1382234 MAGe sequences, MAGK Homo sapiens cDNA
3360	16119	28775	1.3	2.9E-02	AF069063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3360	16119	28776	1.3	2.9E-02	AF069063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5400	18200	30905	11.92	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3048067 5'
6711	19626	32670	1.15	2.8E-02	T78980.1	EST_HUMAN	yt21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108955 5'
8225	20920	34058	1.61	2.8E-02	AJ005820.1	NT	Craterostigma planiginum mRNA for homeodomain leucine zipper protein (hb-1)
8915	21608	34749	0.95	2.8E-02	AA280782.1	EST_HUMAN	zs98c06.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711496 5'
9108	21798	34880	1	2.8E-02	AF187872.1	NT	Carla porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9212	21891	35058	0.99	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R06966.1	EST_HUMAN	Y12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
12630	24876		1.48	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human geminin T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV7S1A1N1T, TCRBV1S3S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV1S3S9/1S3>
1472	14219	26805	1.23	2.7E-02	U06059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3425	18182	28832	1.74	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4178	18918	29545	1.92	2.7E-02	N47268.1	EST_HUMAN	y98h12.r1 Soares multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	18918	29546	1.92	2.7E-02	N47268.1	EST_HUMAN	y98h12.r1 Soares multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:280487 5'
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	yf3009.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
5812	18601	31529	0.86	2.7E-02	X61670.1	NT	T.aestivum p1TH20 mRNA for wheat type V thionin
5885	18671	31612	0.64	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6505	19270		0.93	2.7E-02	X07580.1	NT	A.bisporus pgkA gene
6967	19449	32467	2.29	2.7E-02	AA993571.1	EST_HUMAN	cd96h03.s1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1624661 3'

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8252	20948		1.08	2.7E-02	A1377038.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element
8514	21206	34349	0.49	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 857 nt, segment 4 of 11]
558	13340	26068	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2369	15088	27825	3.29	2.6E-02	AA480021.1	EST_HUMAN	ab02b02.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2368	15090	27827	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hirc), mRNA
2368	15090	27828	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hirc), mRNA
2916	15882		1.88	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4847	17577	30200	2.25	2.6E-02	L12032.1	NT	Chicken drcalrin-1 mRNA, complete cds
5005	17728	30332	1.56	2.6E-02	AE002014.1	NT	Delinococcus radiorans R1 section 151 of 229 of the complete chromosome 1
5032	17752	30384	2.35	2.6E-02	AW241154.1	EST_HUMAN	xs52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5754	18548		0.7	2.6E-02	AL161563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
5800	18580		0.59	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6125	18903		7.34	2.6E-02	A1206030.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Ki68 Homo sapiens cDNA clone IMAGE:1762317 3'
6331	19101	32089	1.9	2.6E-02	BE621748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6728	19562	32593	0.9	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
6728	19562	32594	0.9	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
6810	19471	32494	7.11	2.6E-02	6891271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8403	21096	34232	0.71	2.6E-02	AA860948.1	EST_HUMAN	sk22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9280	22014	35182	1.15	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9814	22267	35453	0.75	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9814	22267	35454	0.75	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10303	22950	36185	4.39	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11191	23856		1.67	2.6E-02	4508486	NT	Homo sapiens radixin (RDX) mRNA
11361	24049		2.33	2.6E-02	AA279351.1	EST_HUMAN	za84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
11553	24162	37465	2.2	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BNO-48-g-10-0-UL1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077466 5'
12170	25375	30615	2.09	2.6E-02	BF343827.1	EST_HUMAN	002015501F1 NCI_CGAP_Brm4 Homo sapiens cDNA clone IMAGE:4150944 5'
519	13303	25935	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
519	13303	25936	1.75	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
791	13563	26224	15.9	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
849	13619	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2768	15471		2.24	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2958	15722	28371	4.35	2.5E-02	X09897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2958	15722	28372	4.35	2.5E-02	X09897.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17879	28389	1	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-080700-001-412 NN0128 Homo sapiens cDNA
4023	17879	29400	1	2.5E-02	BE701185.1	EST_HUMAN	PM2-NN0128-090700-001-412 NN0128 Homo sapiens cDNA
4182	16922	29560	4.23	2.5E-02	AW682114.1	EST_HUMAN	h56h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5625	18422	31335	0.61	2.5E-02	AI732776.1	EST_HUMAN	z683c10.x5 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:810354 3'
6100	18878		5.01	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI_CGAP_Luz4 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1
6115	18993		4.1	2.5E-02	BE746888.1	EST_HUMAN	repetitive element 1;
6244	19018	31982	1.04	2.5E-02	L29029.1	NT	601570333F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3928054 5'
7563	20233	33336	1.7	2.5E-02	BF526722.1	EST_HUMAN	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33337	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34950	0.81	2.5E-02	O81713	SWISSPROT	602070562F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4213406 5'
8863	21554	34869	0.47	2.5E-02	AW025821.1	EST_HUMAN	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9868	22814		0.55	2.5E-02	X71303.1	NT	wu08c10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3'
10482	23128	36356	0.65	2.5E-02	A1147815.1	EST_HUMAN	D. radiatum 28S ribosomal RNA, D2 domain
10712	23401	36940	2.01	2.5E-02	Q10335	SWISSPROT	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1698982 3'
10712	23401	36941	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL_46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10773	23456	36700	2.32	2.5E-02	AJ237836.1	NT	HYPOTHETICAL_46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Bos taurus partial stat5B gene, exons 17-19
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
10795	23478		3.46	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-4>
11770	24361		2.55	2.5E-02	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
12134	25311		2.89	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12311	25182		1.78	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12432	24804	31043	1.94	2.5E-02	BE973327.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3935513 3'
1593	14339	27028	1.7	2.4E-02	H65884.1	EST_HUMAN	y75f11.r1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211149 5'
2037	15584	27501	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27502	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4335	17074	26702	1.65	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4485	17220	28647	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	17220	28648	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5068	17787	30403	0.95	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6121	18899	31807	0.9	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares fetal liver spleen 1NFLS ST1 Homo sapiens cDNA clone IMAGE:416791 3'
6267	19040	32016	0.58	2.4E-02	M31650.1	NT	Chicken myeloblasted alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6267	19040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myeloblasted alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	19809	32875	0.8	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7138	19825	32892	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7138	19825	32893	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7791	20486		0.72	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-106 ST0186 Homo sapiens cDNA
7844	20539		0.5	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8340	21033		0.89	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233578 3' similar to contains Alu repetitive element; contains A3R repetitive element ;
8429	21122	34260	9.78	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294598 3' similar to gb K02809 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element ;
8885	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8907	21598	34740	0.78	2.4E-02	AA625680.1	EST_HUMAN	zu191c08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 SLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element ;
9591	22244	35427	0.52	2.4E-02	AF124100.1	NT	Arabidopsis thaliana molybdopterin synthase sulphuryase (crx5) gene, complete cds
9591	22244	35428	0.52	2.4E-02	AF124100.1	NT	Arabidopsis thaliana molybdopterin synthase sulphuryase (crx5) gene, complete cds
9708	22357	35553	2.38	2.4E-02	AV692854.1	EST_HUMAN	AV692854 GKC Homo sapiens cDNA clone GKCDSC03 5'
9881	22531	35728	2.73	2.4E-02	AA483894.1	EST_HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:343583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
10512	23158		0.46	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815902 5'
11565	24164	37475	1.89	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, Muts homolog, C.OP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11565	24164	37476	1.89	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, Muts homolog, C.OP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11938	24495		2.28	2.4E-02	9827909	NT	Bacteriophage b11.57, complete genome
12081	24589	31124	1.91	2.4E-02	6753635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
12136	24625	31094	2.37	2.4E-02	BE928899.1	EST_HUMAN	MR0-F10175-310800-202-406 F10175 Homo sapiens cDNA
12186	24657	31063	1.68	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12183	24657	31104	1.88	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12216	24678		1.34	2.4E-02	AF163864.1	NT	Homo sapiens SINCA isoform (SNCA) gene, complete cds, alternatively spliced
12380	24764		3.88	2.4E-02	AB008589.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1865	14803		4.29	2.3E-02	W05340.1	EST_HUMAN	z84g08.r1 Somis_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288294 5'
1880	14817		10.45	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2350	15072	27809	2.08	2.3E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3670	16423	29084	6.19	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P, Human foetal Brain Whole tissue Homo sapiens cDNA
3702	16455		0.8	2.3E-02	L23429.1	NT	Carle beta-galactosidase-binding lectin (LGALS3) mRNA, 3' end
4129	16871	29489	1.06	2.3E-02	L24798.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4129	16871	29500	1.06	2.3E-02	L24798.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	29755	0.93	2.3E-02	AW869107.1	EST_HUMAN	CM4-NN0080-297400-180-504 NN0080 Homo sapiens cDNA
4415	17152	29780	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-011800-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-011800-318-g07 MT0118 Homo sapiens cDNA
4416	17880	29782	1.14	2.3E-02	AW593893.1	EST_HUMAN	xs25508.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4416	17880	29783	1.14	2.3E-02	AW593893.1	EST_HUMAN	xs25508.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4555	17290	29819	2.56	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4555	17290	29920	2.56	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5281	18096	30756	3.63	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV PseE subunit (pseE) gene, complete cds, and propionyl-CoA
6522	19288	32292	4.08	2.3E-02	AL161505.2	NT	carboxylesterase beta chain (pccB) homolog gene, partial cds
6883	17859	30513	0.89	2.3E-02	BE141476.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7776	20472	33595	6.28	2.3E-02	U83610.1	NT	MRO-HT0080-071099-002-c09 HT0080 Homo sapiens cDNA
8370	21063	34204	0.94	2.3E-02	AJ298105.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8370	21063	34205	0.94	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34429	0.88	2.3E-02	AF695390.1	EST_HUMAN	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34430	0.88	2.3E-02	AF695390.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9036	21728	34890	0.98	2.3E-02	PA1906	SWISSPROT	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9759	22410	35817	0.77	2.3E-02	P60532	SWISSPROT	HYPOPHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9829	22577	35776	1.33	2.3E-02	AE000199.1	NT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9829	22577	35777	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1685 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Escherichia coli K-12 MG1685 section 89 of 400 of the complete genome
							Bacillus licheniformis isolate N57N1 KexA gene, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10882	23373	38815	2.16	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12058	25186		5.07	2.3E-02	BE278331.1	EST_HUMAN	801179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546587 5'
12562	24892	30967	2.19	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12616	25409		2.42	2.3E-02	U11077.1	NT	Dictyostellium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12807	25260		1.62	2.3E-02	11426388	NT	Homo sapiens dead ringer (Droscophila)-like 1 (DRIL1), mRNA
720	13494	26147	4.13	2.2E-02	AF018287.1	NT	Columbia lily nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1741	14483		1.38	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3428	16185		1.49	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCI_CGAP_Gest1 Homo sapiens cDNA clone IMAGE:1084782 3'
3637	16390		4.01	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3834	16585	29221	1.28	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-17/0100-004-b03 BT0340 Homo sapiens cDNA
3899	16649	29280	0.75	2.2E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5006	17729	30333	1.05	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7146	19833	32902	3.63	2.2E-02	AV699721.1	EST_HUMAN	AV698721 GKB Homo sapiens cDNA clone GKBAND03 3'
8269	20963	34104	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8269	20963	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X70468.1	NT	P. vulgaris alpha t.b 2 mRNA
9586	22239	35422	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9586	22239	35423	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10105	22753		0.89	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11167	23834	37115	1.66	2.2E-02	BE797001.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
11841	24425	37768	1.54	2.2E-02	11423632	NT	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
12315	24737		4.07	2.2E-02	AA603553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
410	13195		6.11	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
436	13222		9.98	2.1E-02	AF029726.1	NT	Dictyostellium discoideum histidine kinase C (dhkC) mRNA, complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	13989	26956	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1366	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1366	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.08	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27492	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2028	14763	27493	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2591	15305	28041	1.32	2.1E-02	AA225085.1	EST_HUMAN	nc21g03.r1 NC1 CGAP P11 Homo sapiens cDNA clone IMAGE:1008820
2819	13534	26183	4.48	2.1E-02	N29286.1	EST_HUMAN	yx43107.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:284541 5'
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
3571	16328	26973	1	2.1E-02	AA461271.1	EST_HUMAN	z03b09.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4110	18653	20480	0.81	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	29641	0.81	2.1E-02	BF343955.1	EST_HUMAN	602015308F1 NC1 CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4151161 5'
4410	17147	29775	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
4421	17157	29788	1.53	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4481	17197		0.69	2.1E-02	Y19213.1	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
4692	17396	30031	4.91	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL163302.2	NT	Homo sapiens chromosome 21: segment HS21C102
4769	17501	30124	0.76	2.1E-02	A1829432.1	EST_HUMAN	wh54e05.x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2384528 3'
5553	18350	31259	1.13	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111196-040-H05 HT0244 Homo sapiens cDNA
6968	19448	32468	0.88	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120000-329-012 GN0058 Homo sapiens cDNA
8417	21110	34249	0.6	2.1E-02		NT	Mus musculus coding region 1 (Snrl1), mRNA
9403	22065	35236	0.5	2.1E-02	AA984288.1	EST_HUMAN	am83e07.a1 Strabigene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9531	22184	35368	2.61	2.1E-02	AJ243213.1	NT	Alu repetitive element contains element MER11 repetitive element;
9531	22184	35369	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
						NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9983	22533	35730	1.15	2.1E-02	L28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
9961	22609	35814	0.69	2.1E-02	AA984288.1	EST_HUMAN	am83e07.a1 Strabigene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
10522	23168	36395	0.45	2.1E-02	AP001519.1	NT	Alu repetitive element contains element MER11 repetitive element;
						NT	Bacillus halodurans genomic DNA, section 13/14

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11479	24080	37391	1.38	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp60a), mRNA
12296	17197		8.62	2.1E-02	Y19213.1	NT	Homo sapiens putative peptidase pseudogene for hair keratin, exons 2 to 7
12339	25163	30901	1.89	2.1E-02	L34170.1	NT	Human geminine UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30969	5.71	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
16	12844	26457	1.1	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:3309908 3' similar to contains MER1.13
17	12845	25458	14.4	2.0E-02	AW89595.1	EST_HUMAN	MER1 repetitive element;
252	13061	25689	3.76	2.0E-02	6753635	NT	QV4-NN0038-270400-167-h05 NN0038 Homo sapiens cDNA
288	13094	25736	2.72	2.0E-02	AA456638.1	EST_HUMAN	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
781	13553	26214	2.11	2.0E-02	6753635	NT	Est15b10.1 Soerries_NHMPu_S1 Homo sapiens cDNA clone IMAGE:313307 5'
1065	13823	26483	1.8	2.0E-02	AL068805.1	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
1177	13830	26595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1177	13830	26596	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1896	14604	27313	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1896	14604	27314	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15506		3.24	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3077	12844	26457	2.11	2.0E-02	BF002832.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3141	15905			2.0E-02			7g51c08.x1 NCJ_CGAP_P728 Homo sapiens cDNA clone IMAGE:3309908 3' similar to contains MER1.13
3221	15984		1.4	2.0E-02	7305474	NT	MER1 repetitive element;
3588	18736	29370	2.35	2.0E-02	AF085588.1	NT	Mus musculus aema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sem6b), mRNA
5548	18345	31254	0.58	2.0E-02	U34778.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5807	18598	31523	0.7	2.0E-02	L35321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7460	20126	33217	1.11	2.0E-02	AP000004.1	NT	Caenorhabditis elegans smc-2 mRNA, complete cds
7450	20128	33218	1.11	2.0E-02	AP000004.1	NT	Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds
9777	22428		2.21	2.0E-02	U70406.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (477)
10269	22907	36117	1.82	2.0E-02	A1840342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (477)
10539	23236	36489	1.78	2.0E-02	D73996.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	wat17b02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288316 3'
11882	24277	37698	2.21	2.0E-02	10947056	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/192
11882	24277	37589	2.21	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
							Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
							Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11860	17809	30595	1.9	2.0E-02	AA458638.1	EST_HUMAN	aat15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12336	15008		1.82	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	26038		6.4	2.0E-02	T80037.1	EST_HUMAN	y04c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24875 5'
677	13452	28095	2.15	1.9E-02	AA572764.1	EST_HUMAN	ntf18a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.t1 L1 repetitive element:
1611	14358	27047	1.15	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27406	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2032	14767	27497	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2310	15227	27968	0.97	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2906	15872	28320	7.48	1.9E-02	AA713858.1	EST_HUMAN	mw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1288337 3'
2952	15718	28369	1.66	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3588	16351		1.18	1.9E-02	N52250.1	EST_HUMAN	y228f02.s1 Soares_multiple_sclerosis_2N1bHMP Homo sapiens cDNA clone IMAGE:284331 3'
3681	16444		9.58	1.9E-02	BE738088.1	EST_HUMAN	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3703	19456	28095	0.95	1.9E-02	AI301183.1	EST_HUMAN	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element:
4025	16770	29402	1.49	1.9E-02	AF141940.1	NT	Myoplasma lititans VhaA1 precursor (vhaA1) and VhaA2 precursor (vhaA2) genes, partial cds
4170	16910	29539	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4170	16910	29540	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	29872	3.21	1.9E-02	AI452999.1	EST_HUMAN	y46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element
4951	15227	27898	4.09	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
6233	18039	30667	0.99	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
6382	18182	30872	1.41	1.9E-02	L47572.1	NT	Meleagris gallopavo paracetamol-2 (PON2) mRNA, complete cds
6701	18495		0.86	1.9E-02	AB016507.1	NT	Drosophila keratins gene for glyceral-3-phosphate dehydrogenase, complete cds
7001	19693	32744	1.38	1.9E-02	U16241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7001	19693	32745	1.38	1.9E-02	U16241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469	21161		1.23	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9230	21909	35082	1.03	1.9E-02	BF316129.1	EST_HUMAN	601806130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3125462 5'
9613	22286	35452	0.6	1.9E-02	LI10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9645	22593	35796	1.05	1.9E-02	BF698632.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10152	22800	36017	0.54	1.9E-02	D04001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2839000-2844794
10681	23372	36614	1.44	1.9E-02	AF008038.1	NT	Vibrio cholerae V861 phage putative replication protein gene, complete cds
12090	25171	30903	2.82	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gillrin mRNA, complete cds
12646	25147		1.36	1.9E-02	LI11068.1	NT	Candida albicans kmbda Ca3B fragment

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
338	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	h152c06.x1 NCI_OGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
670	13448	26086	0.83	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138983 5'
1137	13892	26553	1.32	1.8E-02	X17064.1	NT	H. fransisci mRNA for myelin basic protein (MBP)
1416	14104	26947	1.73	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
2685	15304	28133	1.71	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 106 of 529 of the complete genome
3205	15998		0.94	1.8E-02	A1805829.1	EST_HUMAN	h62a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080296 3'
4065	16810		0.99	1.8E-02	AA861448.1	EST_HUMAN	sk24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3'
4398	17133	20764	1.17	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
6712	19827	32671	5.02	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
8029	20724	33857	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8367	21060	34200	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-168-h09 NN1073 Homo sapiens cDNA
8410	21103	34242	0.8	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA
9392	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9392	22064	35226	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9542	22195		2.41	1.8E-02	AA897543.1	EST_HUMAN	aj6209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9963	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869983 5'
10128	22774	35987	1.37	1.8E-02	X96933.1	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11613	24211	37535	1.59	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1186001-1485000 nt position (8/7)
11628	24223	37545	3.32	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
886	13555	26323	1.86	1.7E-02	BE394869.1	EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1783	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
1783	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
1864	14602		3.41	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2106	14637		10.5	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitisugmin29, complete cds
2291	15016	27762	0.99	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2646	15358		1.01	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2696	15762	28411	1.44	1.7E-02	AI147815.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1869892 3'

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3502	16288		4.97	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3614	16367		0.73	1.7E-02	P04929	SWISSPROT	MER19.b1 MER19 repetitive element;
4148	16930		1.23	1.7E-02	AA069618.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4176	16916		2.04	1.7E-02	R02506.1	EST_HUMAN	ac19f04.s1 Stratigene ovary (#637217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4420	17156	28787	1.49	1.7E-02	A1305279.1	EST_HUMAN	ye88f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4491	17227	29858	1.78	1.7E-02	AW573183.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4666	17400	30034	1.91	1.7E-02	V00841.1	NT	hm34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
4763	17495		5.84	1.7E-02	A1015076.1	EST_HUMAN	Messenger RNA for anglerfish ( <i>Lopholatilus chamaeleonis</i> ) somatostatin II
5007	17730	30334	0.69	1.7E-02	6981286	NT	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5096	17915		0.91	1.7E-02	AJ229041.1	NT	Rattus norvegicus N-arginine diisic convertase 1 (Nrd1), mRNA
6035	18615	31775	2.07	1.7E-02	A1766247.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21 q22; segment 1/3
6484	19251	32250	1.47	1.7E-02	A1038280.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6950	19432	32448	1.27	1.7E-02	AF190830.1	NT	oy95h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7103	19791	32856	2.44	1.7E-02	8400716	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7267	19941	33016	1.06	1.7E-02	L07899.1	NT	Homo sapiens nebulin (NEB), mRNA
7267	19941	33017	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7642	20307		1.78	1.7E-02	AJ010770.1	NT	Human apolipoprotein (a) gene, exon 1
9336	20407	33523	0.98	1.7E-02	U21854.1	NT	Homo sapiens hyperion gene, exons 1-50
9598	22251	35437	1.3	1.7E-02	AL040554.1	EST_HUMAN	Caenorhabditis elegans cCAF1 protein gene, complete cds
11801	24391	37724	1.38	1.7E-02	5802007	NT	DKFZp434i0314.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434i0314 5'
12631	26337	30716	2.39	1.7E-02	AW903482.1	EST_HUMAN	Homo sapiens serpin constituent protein (MSE65), mRNA
498	13282		3.19	1.6E-02	AL021929.1	NT	GM4-NN1030-040-400-130-408 NN1030 Homo sapiens cDNA Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1653	14390	27088	1.04	1.6E-02	Y18899.1	NT	Treponema maltophilum flaB2, flaB3 and flid genes for flagellin subunit proteins and CAP protein homologues
2246	14974	27711	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.9	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2649	15359	28102	1.48	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2699	15408		0.96	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3016	15792	28431	0.71	1.0E-02	AF112282.1	NT	Laccase sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28028	5.9	1.0E-02	AW850652.1	EST_HUMAN	IL3-CT0219-16:200-063-C07 CT0219 Homo sapiens cDNA
3830	16581	28215	1.32	1.0E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4154	16898		2.49	1.0E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4267	17007	29840	0.97	1.0E-02	AW875407.1	EST_HUMAN	QV2-P10012-140100-030-f07 P10012 Homo sapiens cDNA
5536	18334	31241	1.25	1.0E-02	8671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
5548	19311	32316	2.05	1.0E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6832	19494	32517	1.75	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	0.98	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33847	0.76	1.0E-02	AJ277062.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8078	20772		1.98	1.0E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
9940	22588		2.72	1.0E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22986	36184	1.29	1.0E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29284 TELOKIN. [1];
10319	22986	36185	1.29	1.0E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29284 TELOKIN. [1];
10826	25132	36748	2.38	1.0E-02	Z94928.1	NT	G gallus microsatellite DNA (LE10260 (=T161E11))
11174	23841	37124	2.54	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11174	23841	37125	2.54	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11495	24096	37407	1.54	1.0E-02	AJ373558.1	EST_HUMAN	qz99e10.x1 Soarans_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
734	13508		23.05	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2138	14888	27598	4.24	1.5E-02	N39821.1	EST_HUMAN	yv27b07.s1 Soarans fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:243825 3'
2172	14901	27635	1.69	1.5E-02	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3057	15823	28467	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3057	15823	28468	1.6	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3711	16464	29103	0.98	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
6201	18977	31955	1.58	1.5E-02	Q09711	SWISSPROT	HYPOPHOSPHATE CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7219	19904		1.63	1.5E-02	11467282	NT	Cyanophora paradoxa cyanella, complete genome
7301	19984	33060	1.2	1.5E-02	11418713	NT	Homo sapiens KIA1009 protein (KIAA1009), mRNA

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20469	33592	1.63	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20476	33602	3.59	1.5E-02	11417739	NT	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
8729	21421	34565	0.9	1.5E-02	BF345554.1	EST_HUMAN	802019135F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4154504 5'
8368	21943		0.61	1.5E-02	AF008774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22079	35251	1.47	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9711	22362	35559	0.98	1.5E-02	R32687.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.98	1.5E-02	R32687.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23790	37068	3.49	1.5E-02	L40009.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11163	23830	37109	2.14	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11856	24440	37781	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	26214		1.74	1.5E-02	AW780834.1	EST_HUMAN	RC4-CN0049-14/100-011-c11 CN0049 Homo sapiens cDNA
12787	25039		1.45	1.5E-02	A1763127.1	EST_HUMAN	wf0803.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element;
408	13193		2.29	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1096	13854	26513	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13983		1.24	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1375	14123		1.45	1.4E-02	AF218954.1	NT	Homo sapiens hesdin gene, complete cds
1607	14263		1.26	1.4E-02	AV723786.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3207	15970	28622	2	1.4E-02	AF160699.2	NT	Bifidobacterium longum Nev/H+ antiporter (nhab), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminyl/xylose repressor protein (nagCxyIR) gene, partial cds
3393	16162	28805	1.07	1.4E-02	AW074212.1	EST_HUMAN	xd0809.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575783 3'
3478	16234	28898	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28899	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3648	16401	29041	8.63	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29817	7.77	1.4E-02	AW902868.1	EST_HUMAN	EST374761 MAGG: resequences, MAGG Homo sapiens cDNA
4455	17191	29818	7.77	1.4E-02	AW902868.1	EST_HUMAN	EST374761 MAGG: resequences, MAGG Homo sapiens cDNA
4821	17552	30174	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	18091	32079	5.47	1.4E-02	AA559030.1	EST_HUMAN	nh1104.s1 NCI_C3AP_Br2 Homo sapiens cDNA clone IMAGE:1028990 3' similar to contains Alu repetitive element;

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	19091	32080	5.47	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029890 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8798	21488	34634	0.75	1.4E-02	M81702.1	NT	Candida boldini methylated oxidase (AOD1) gene, complete cds
9053	21742	34900	0.84	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11985	24526	37267	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12601	24913		2.36	1.4E-02	11428968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27395	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF169288.1	NT	Mus musculus beta-actin gene, complete cds
4874	17601	30223	0.83	1.3E-02	U66001.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBU1S1, TCRBU1S2, >
5166	17975	30532	1.31	1.3E-02	AL048886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, rrmxq28orf
5166	17975	30533	1.31	1.3E-02	AL048886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, rrmxq28orf
6072	18851	31816	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6105	18883	31851	0.88	1.3E-02	M62982.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6865	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6865	17942	30536	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7477	20150	33244	4.9	1.3E-02	AK031503.1	EST_HUMAN	on060605.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8380	21073	34212	1.85	1.3E-02	AF169661.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107	22755	35987	1.91	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22826	36040	0.68	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10913	23593	36938	3.97	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36939	3.97	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12337	25352		1.44	1.3E-02	Z98117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12437	24807		2.41	1.3E-02	9633068	NT	Human herpesvirus 6B, complete genome
12807	25145		28.18	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	25783	3.48	1.2E-02	AA050209.1	EST_HUMAN	z86g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element
440	13228	25809	1.66	1.2E-02	P38808	SWISSPROT	L1 repetitive element;
721	13405						HYPOPHYSICAL 17.1 KD PROTEIN IN PUR5 3'REGION
2176	14904	28148	2.02	1.2E-02	AI183522.1	EST_HUMAN	gc68a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1.L1 L1
2178	14907	27637	1.81	1.2E-02	AL183213.2	NT	repetitive element;
2444	15163	27840	1.71	1.2E-02	AV731704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2642	15163	27901	1.39	1.2E-02	AW172350.1	EST_HUMAN	AV731704 HTF -Homo sapiens cDNA clone HTFBHG11 5'
3098	15903	27901	1.07	1.2E-02	AW172350.1	EST_HUMAN	x37c09.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859432 3'
3281	16042	28601	6.68	1.2E-02	AA075418.1	EST_HUMAN	x37c09.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859432 3'
3284	16045	28694	2.1	1.2E-02	R62805.1	EST_HUMAN	zm88a03.r1 Siratogene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:545020 5'
4675	17409	30045	0.92	1.2E-02	AI938694.1	EST_HUMAN	y11508.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
			0.91	1.2E-02	AI887378.1	EST_HUMAN	zb06a07.x5 Soares_fetal_kurq_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
							wm39f04.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2498335 3'
4859	17588	30211					
4881	17704		2.03	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
6025	17748	30358	1.13	1.2E-02	AB019788.1	NT	Cynops pyrrhogaster CpUbgT mRNA, partial cds
5006	18461	31375	1.41	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
6028	18806	31787	1.73	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6907	19645	32891					Homo sapiens wbcscr1 (WBSCR1) and wbcscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7192	19878	32952	0.72	1.2E-02	AF045555.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, complete cds
7212	19897	32972	6.46	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7456	20130	33222	1.36	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBUC09 5'
			10.54	1.2E-02	BF216850.1	EST_HUMAN	601882949F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4065253 5'
			0.57	1.2E-02			CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
7896	20591	33722					Homo sapiens frings protein mRNA, partial cds
8092	20786	33917	2.18	1.2E-02	Q11206	SWISSPROT	Homo sapiens frings protein mRNA, partial cds
8092	20786	33918	1.35	1.2E-02	AF193612.1	NT	Homo sapiens frings protein mRNA, partial cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8788	21480		1.03	1.2E-02	T76987.1	EST_HUMAN	yf72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35376	2.46	1.2E-02	AB031013.1	NT	Norwalk-like virus group 2 gene for capsid protein, complete cds
9570	22223	35408	1.35	1.2E-02	AJ246003.1	NT	Homo sapiens S100t gene for spectrin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)
12615	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujivara) Homo sapiens cDNA clone GEN-557G06 5'
1246	13995	26662	1.49	1.1E-02	AA070394.1	EST_HUMAN	zmf80e11.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1701	14444	27143	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2031	14766	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2880	15647		4.06	1.1E-02	N99623.1	EST_HUMAN	z440e06.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286040 5'
3513	16269	26624	2.98	1.1E-02	A1653508.1	EST_HUMAN	tg95b10.x1 NC1 CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW-XPF_HUMAN
4086	16829		0.86	1.1E-02	AW813786.1	EST_HUMAN	Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30132	1.5	1.1E-02	AL048983.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp588E0924_s1 588 (synonym: huter) Homo sapiens cDNA clone DKFZp588E0924
6057	18837	31789	1	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spvK), YnbA (ynbA), YnbB (ynbB), GhrR (ghrR), glutamine synthetase (ghsA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl
7497	20169	33261	2.51	1.1E-02	BE148611.1	EST_HUMAN	RC1-HT0256-100300-018-H07 HT0256 Homo sapiens cDNA
8638	21230	34372	0.91	1.1E-02	AW908180.1	EST_HUMAN	QV3-BN0045-220300-128-H02 BN0045 Homo sapiens cDNA
8721	21413	34558	0.67	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
8800	21492	34639	6.45	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9828	22480	35682	2.03	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.t1 Stratiogene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9994	22842	35854	3.55	1.1E-02	AA314665.1	EST_HUMAN	EST188494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10900	23580	36830	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11923	24484		4.18	1.1E-02	AA668239.1	EST_HUMAN	ab7711.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12078	16829		1.62	1.1E-02	AW813786.1	EST_HUMAN	Alu repetitive element
6	12833	25448	9.18	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1513	14280	26946	1.56	1.0E-02	AW398128.1	EST_HUMAN	MR3-CT0176-111069-003-g10 CT0176 Homo sapiens cDNA
2577	15291		1.57	1.0E-02	AA808389.1	EST_HUMAN	CM2-HT0177-041098-017-H12 HT0177 Homo sapiens cDNA
3087	15852	28494	2.7	1.0E-02	BE835558.1	EST_HUMAN	cc22f08.s1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350485 3'
3257	16019	28669	1.49	1.0E-02	BE889999.1	EST_HUMAN	RCO-FN0025-250400-021-d02 FN0025 Homo sapiens cDNA
3361	16611	29250	0.79	1.0E-02	AI095086.1	EST_HUMAN	60184987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833689 3'
							HA0921 Human fetal liver cDNA library Homo sapiens cDNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3876	16626	29284	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4726	17458	30094	4.24	1.0E-02	0753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr12), mRNA
4793	17524	30146	5.16	1.0E-02	R95667.1	EST_HUMAN	yq54h01.r1 Soeris fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5331	18134	30793	0.72	1.0E-02	H52681.1	EST_HUMAN	yq36h11.r1 Soeris ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:235941 5'
5961	18456	31370	0.57	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6025	18805	31786	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptobrevin II (Sy2) gene, complete cds
6088	18866	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT03568-070100-201-h01 BT03568 Homo sapiens cDNA
6088	18866	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT03568-070100-201-h01 BT03568 Homo sapiens cDNA
6664	19581	32616	1.92	1.0E-02	Z26842.1	NT	Z.mays U3snRNA pseudogene
9293	21980	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	601456570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9293	21980	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	601456570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11229	23892		1.97	1.0E-02	AF157559.1	NT	Griffithia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11263	23925		1.46	1.0E-02	A1417961.1	EST_HUMAN	ig55h07.x1 NCL_C3GAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:U15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element:
11340	24030	37334	1.97	1.0E-02	A1417961.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12003	25416	382203	1.83	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12059	25189	30811	3.78	1.0E-02	AW635521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12075	25243		5.93	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12582	25289		3.74	1.0E-02	X62654.1	NT	H. sapiens gene for Me49/CD63 antigen
12803	25050	30957	1.84	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
873	13642	26312	2.1	9.0E-03	A1796126.1	EST_HUMAN	WH42R9.x1 NCL_C3GAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element:
1241	13980		2.07	9.0E-03	BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
1463	14211	26899	1.1	9.0E-03	AE001270.1	NT	Treponema pallidum section 86 of 87 of the complete genome
2394	15115	27852	2.48	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2403	15124	27861	0.92	9.0E-03	AF099934.1	NT	Mus musculus MHC class III protein RP1 (Rpr1) mRNA, partial cds
3659	16412	23050	1.21	9.0E-03	J05184.1	NT	S. acidocaldarius thermopain gene, complete cds
4927	17655	30267	1.03	9.0E-03	BE047849.1	EST_HUMAN	tz44e10.y1 NCL_C3GAP_Bm52 Homo sapiens cDNA clone IMAGE:2291466 5'
4964	17689	30297	0.95	9.0E-03	T70044.1	EST_HUMAN	yq17b08.st1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
4984	17689	30298	0.95	9.0E-03	T70044.1	EST_HUMAN	yq17b08.st1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
5720	18512		1.15	9.0E-03	A1809792.1	EST_HUMAN	wf7704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
9533	19299		4.88	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7362	20043	33122	0.57	9.0E-03	AI242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7371	20051	33132	0.8	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10850 (FLJ10850), mRNA
7774	20470		1.05	9.0E-03	AL036901.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8147	20841		0.65	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
9745	22398	35601	0.47	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M260 IEL ANTIGEN)
9782	22413	35620	1.44	9.0E-03	P20808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10907	23587		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10935	23615	38866	1.57	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens priprogalactin (GAL1) gene, exons 1, 2, and 3
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens priprogalactin (GAL1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.48	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0462-281-289-001-e09 HT0462 Homo sapiens cDNA
489	13274		4.06	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pheal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413586 3' similar to contains Alu repetitive element
998	13734	26399	36.32	8.0E-03	AF106658.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2154	14884	27617	2.2	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2980	15726		0.93	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3353	16113	28768	1.08	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3665	16418	28058	1.21	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3665	16418	28059	1.21	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4350	17089	28721	4.88	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0719-300600-223-b05 NN0719 Homo sapiens cDNA
5083	17802	30420	1.09	8.0E-03	AU140261.1	EST_HUMAN	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
6436	18235	30949	2.82	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, leucine, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6106	25085	31852	1.45	8.0E-03	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (277)
6651	19413	32427	4.89	8.0E-03	P35577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6820	19481		0.95	8.0E-03	V01106.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19795	32860	1.79	8.0E-03	M17197.1	NT	A californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038267.1	NT	Turkops truncatus mRNA for p40-phox, complete cds
8781	21473	34619	0.63	8.0E-03	P98180	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8808	21500	34646	3.29	8.0E-03	AW808992.1	EST_HUMAN	MR1-ST0111-111199-011-H06 ST0111 Homo sapiens cDNA
8816	21508	34693	0.49	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/8
8878	21569	34713	0.58	8.0E-03	9789958	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
8848	22488		4.63	8.0E-03	BE089509.1	EST_HUMAN	QV1-BT0677-040-400-131-g03 BT0677 Homo sapiens cDNA
10906	23357	36597	1.36	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
10008	23586		3.58	8.0E-03	Z49652.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
11715	24309	37632	4.74	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11814	24402		22.71	8.0E-03	AA018180.1	EST_HUMAN	z832e11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360716 5'
11853	24437	37779	1.36	8.0E-03	BF342436.1	EST_HUMAN	602013941F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4149418 5'
11933	24491		1.74	8.0E-03	M89035.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
11980	24523		1.74	8.0E-03	AB038161.1	NT	Homo sapiens AB CG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13483	26098	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
678	13453	26097	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
956	13721	26387	3.57	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1094	13852	26511	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.87	7.0E-03	Q61080	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1374	14122	26797	5.71	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
1491	14238	26924	3.37	7.0E-03	AW303598.1	EST_HUMAN	ab79608.s1 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:863145 3'
1735	14477	27175	1.24	7.0E-03	AW950556.1	EST_HUMAN	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27176	1.24	7.0E-03	AW950556.1	EST_HUMAN	EST362626 MAGE resequences, MAGE Homo sapiens cDNA
2254	15939	27722	1.86	7.0E-03	P04929	SWISSPROT	EST362626 MAGE resequences, MAGE Homo sapiens cDNA
3546	16301	28951	0.71	7.0E-03	AI150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3749	16502	29137	0.8	7.0E-03	AW444463.1	EST_HUMAN	qf34h02.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3792	16544	29179	1.32	7.0E-03	AF186344.1	NT	UI-H-B13-alk-c-10-JUJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4000	16502	29137	0.83	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4560	17296		1.24	7.0E-03	AW630888.1	EST_HUMAN	UI-H-B13-alk-c-10-JUJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4929	17657		2.17	7.0E-03	AL163278.2	NT	hh89a05.y1 NCI_CGAP_GUI1 Homo sapiens cDNA clone IMAGE:2869836 5'
5729	18521		0.75	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6021	25083		4.9	7.0E-03	AW861059.1	EST_HUMAN	w82g01.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6222	18986	31972	1.47	7.0E-03	W68251.1	EST_HUMAN	gb-X14728 CLUSTERIN PRECURSOR (HUMAN);
							RC1-CT0286-06040-018-c08 CT0286 Homo sapiens cDNA
							z833f10.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6443	19211	32207	3.44	7.0E-03	AA327129.1	EST_HUMAN	EST30874 Colon 1 Homo sapiens cDNA 5' and
6470	19237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NCI_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6879	19504	32529	1.87	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D6_2 contains TAR1.2 TAR1 repetitive element ;
7420	20097	33184	5.48	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175687.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBL077w
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9297	21984		0.75	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9495	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9620	22273	35480	2.67	7.0E-03	P48982	SWISSPROT	y44010.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9620	22273	35461	2.57	7.0E-03	P48982	SWISSPROT	Alu repetitive element
10204	22852		1.32	7.0E-03	AV987378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10384	23030		0.77	7.0E-03	A198734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10729	23417	36658	2.63	7.0E-03	AB008852.1	NT	AV687379 GKQ Homo sapiens cDNA clone GKCAFO7 5'
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCI_OGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10818	23501	36740	1.71	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
10962	23657		1.29	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12468	24833		1.79	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12553	24890		1.81	7.0E-03	BE283253.1	EST_HUMAN	Sporobolus stipitatus mRNA for putative glycine and proline-rich protein
12681	25400		1.72	7.0E-03	Y17455.1	NT	601145184F2 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
1218	13999	26837	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSF2 gene, penultimate exon
1218	13999	26838	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	h22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2893	15690	28305	3.36	6.0E-03	AA758135.1	EST_HUMAN	SW_PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2893	15690	28306	3.36	6.0E-03	AA758135.1	EST_HUMAN	SW_PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR ;
3240	16002		2.22	6.0E-03	H75690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
3298	16060		1.31	6.0E-03	AF180336.1	NT	sh78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
3377	16136	28783	1.18	6.0E-03	U90690.1	NT	sh78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							y777N04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
							Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
							Fugu rubripes zinc finger protein, isoform, fatty acid binding protein, sepiapterin reductase and vasodilator
							genes, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3377	16138	28794	1.18	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, lectocin, fatty acid binding protein, sepiapterin reductase and vasodilator genes, complete cds
3534	16290		1.19	6.0E-03	W37985.1	EST_HUMAN	zz13a11.1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:322172 5'
3652	16405	23044	3.88	6.0E-03	BF510988.1	EST_HUMAN	U1-H-B14-epm-o-16-O-UJ.1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3682	16435	29078	1.08	6.0E-03	BE077356.1	EST_HUMAN	RC1-B10606-200400-014-007 BT0606 Homo sapiens cDNA
3759	16511	29147	1.22	6.0E-03	6754029	NT	Mus musculus glucosamine-9-phosphatase deaminase (Gnpl), mRNA
3902	16652	29264	0.78	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240009-021-b10 CT0204 Homo sapiens cDNA
3938	16686		1.29	6.0E-03	BE250108.1	EST_HUMAN	600842904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4331	17070		1.84	6.0E-03	AI016833.1	EST_HUMAN	ov33c11.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4647	17381	30013	6.67	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Carab-alkum II Homo sapiens cDNA 5' end similar to EST containing Akl repeat
5073	17782	30407	2.58	6.0E-03	Q62208	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
6061	25084	31802	0.87	6.0E-03	9827521	NT	Varicella virus, complete genome
6718	19833	32676	1.16	6.0E-03	O14904	SWISSPROT	SYNAPSIN III
6755	17924	30559	0.57	6.0E-03	BE253748.1	EST_HUMAN	60112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	19836	32905	0.61	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7149	19836	32906	0.61	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7546	20216	33318	0.89	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-10 and complete cds
7702	20365	33479	0.62	6.0E-03	P17894	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7757	20453	33578	6.9	6.0E-03	AI033980.1	EST_HUMAN	ow13a04.x1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MIER10.b1 MER10 repetitive element;
7874	20589	33695	2.17	6.0E-03	AW798337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7945	20840		1.58	6.0E-03	BF038108.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858628 5'
9454	22004	35176	7.26	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9943	22591		2.13	6.0E-03	AI432681.1	EST_HUMAN	122c02.x1 NCI_OGAP_Kd11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10062	22710	35928	0.86	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
10194	22842		1.14	6.0E-03	AF084555.1	NT	Bacillus subtilis fcrD gene
10304	22951	36186	0.59	6.0E-03	X68368.1	NT	cds
10645	23336	36575	1.75	6.0E-03	AW962164.1	EST_HUMAN	M.thermoformicicum complete plasmid pFV1 DNA
10713	23402		2.54	6.0E-03	11545814	NT	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
10750	23435	36680	1.26	6.0E-03	AI420786.1	EST_HUMAN	Homo sapiens hypopharyngeal zinc finger protein FLJ14011 (FLJ14011), mRNA
							1691c12.x1 NCI_OGAP_P128 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519
							FATTY ACID AMIDE HYDROLASE ;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23435	30681	1.26	6.0E-03	AI420786.1	EST_HUMAN	bs91ct12x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 000519
10903	23583		4.6	6.0E-03	U14558.1	NT	FATTY ACID AMIDE HYDROLASE.
10904	23584	36833	2.81	6.0E-03	BE737895.1	EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
12042	24563		3.25	6.0E-03	AF010496.1	NT	601572746F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839747 5'
12160	25174		6.69	6.0E-03	AE000833.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12239	25235		3.17	6.0E-03	U30790.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450268 (section 39 of 149) of the complete genome
12569	24988		1.64	6.0E-03	BE788019.1	EST_HUMAN	Pneumocystis carinii f. sp. reidi guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12598	24910		1.68	6.0E-03	AJ245480.1	NT	601482621F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3885388 5'
654	13432	26072	2.7	5.0E-03	L25105.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
654	13432	26073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1080	13848	28507	1.15	5.0E-03	AJ010457.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
2688	15397	28135	2.5	5.0E-03	AB033006.1	NT	Arabidopsis thaliana mRNA for KIAA1180 protein, partial cds
2836	15702	28351	0.88	5.0E-03	BE266057.1	EST_HUMAN	Homo sapiens mRNA for KIAA1180 protein, partial cds
3133	15898	28543	3.82	5.0E-03	T87623.1	EST_HUMAN	601194796F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3538766 5'
3152	15915		2.83	5.0E-03	AL161491.2	NT	yc81f09.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3184	15927	28575	1.3	5.0E-03	R71794.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3272	16033		1.12	5.0E-03	AJ297357.1	NT	y88g02.s1 Soares breast 2NBH8at Homo sapiens cDNA clone IMAGE:155868 3'
3687	19440	29082	4.03	5.0E-03	AF147449.2	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3741	18494	29129	0.85	5.0E-03	U39914.1	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3954	16704		1.17	5.0E-03	AA298075.1	EST_HUMAN	Citrus sinensis seed storage protein citrin mRNA, complete cds
4272	18494	29129	0.82	5.0E-03	U39914.1	NT	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' and
4569	17304	29831	0.73	5.0E-03	AJ131016.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4670	17404	30039	1.17	5.0E-03	AJ752387.1	EST_HUMAN	Homo sapiens SGL gene locus
5707	18501	31422	5.5	5.0E-03	P35500	SWISSPROT	on15c02x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
							SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5953	18735	31894	2.97	5.0E-03	O00507	SWISSPROT	PROBABLE UBQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBQUITIN THIOLESTERASE FAF-Y) (UBQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBQUITIN-SPECIFIC PROTEASE 9, Y-CHROMOSOMAL)
5988	18708		0.91	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
8409	18284		7.86	5.0E-03	BE300091.1	EST_HUMAN	800844564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6746	17816	30578	7.45	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for 3'-adenosylmethionine decarboxylase, complete cds
6940	19422		0.64	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7385	20085	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST T03012 Fetal brain, Striatum (cat#036206) Homo sapiens cDNA clone HIFBOR93 similar to EST containing Alu repeat
7498	20170		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031098-011-407 CT0255 Homo sapiens cDNA
7667	20331	33442	7.6	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8119	20813	33048	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.49	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33965	3.29	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8509	21201		5.63	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA (19.1 - 19.4 min)
8838	21530	34676	0.71	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9482	22135	35316	0.45	5.0E-03	P33750	SWISSPROT	SOF1 PROTEIN
9739	22360	35595	0.89	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9871	22821	35716	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA633143.1	EST_HUMAN	h46h10.s1 NCI_CGAP_P99 Homo sapiens cDNA clone IMAGE:865587
10231	22879	36091	0.51	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10377	23023		0.48	5.0E-03	AA633261.1	EST_HUMAN	ag49c10.s1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1128290 3'
10621	23314		4.99	5.0E-03	T19588.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	zn56g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	zn56g05.x1 Soares_NHCC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element
10971	23647	36900	1.89	5.0E-03	T49153.1	EST_HUMAN	y608e04.r1 Stratiotes placenta (#637225) Homo sapiens cDNA clone IMAGE:70688 5'
11021	23693	36956	1.47	5.0E-03	10946753	NT	Mus musculus hypodermal protein, MNCB-4760 (LOC58212), mRNA
11303	23962		3.54	5.0E-03	BE048055.1	EST_HUMAN	tz48c04.y1 NCI_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2281622 5'
11774	24366	37697	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24366	37698	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12176	25367		9.26	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12409	24792		2.52	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12441	24811		1.67	5.0E-03	AA456997.1	EST_HUMAN	zxf5a03.s1 Soeris ovary tumor NibHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to
12467	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	SW:DXA2_MOUSE P1 4895 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12643	24940	30980	4.2	5.0E-03	AW449109.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12662	25263		1.76	5.0E-03	Q02388	SWISSPROT	UI-H-B13-aid-f08-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
226	13038	25675	2.98	4.0E-03	AW500196.1	EST_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
313	13117	25755	2.29	4.0E-03	R48482.1	EST_HUMAN	UI-HF-BNO-alc-1-04-0-J1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078931 5'
589	13369	25997	2.69	4.0E-03	AA939339.1	EST_HUMAN	y51a04.s1 Soeris infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
857	13628	26298	2.03	4.0E-03	R48482.1	EST_HUMAN	on75g12.s1 Soeris_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1662566 3'
881	13680		4.64	4.0E-03	AW749101.1	EST_HUMAN	y51a04.s1 Soeris infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
1128	13884	26544	29.46	4.0E-03	AA099777.1	EST_HUMAN	RC3-BT0333-11C100-012-01 BT0333 Homo sapiens cDNA
1146	13901	26563	2.4	4.0E-03	AW794740.1	EST_HUMAN	z81a08.r1 Stratiogene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
1280	14030	26699	1.57	4.0E-03	AA284374.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1581	14327		1.52	4.0E-03	AV708305.1	EST_HUMAN	z85a01.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:701736 5'
1737	14479	27178	2.23	4.0E-03	U33472.1	NT	AV708305 ADC Homo sapiens cDNA clone ADCAKB08 5'
2011	14746	27474	10.58	4.0E-03	AA099777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and olfactory-imbic associated protein AT1-46 mRNA, complete cds
2244	14972		2.49	4.0E-03	BE410558.1	EST_HUMAN	z81a08.r1 Stratiogene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
2276	15002	27742	1.84	4.0E-03	AW794740.1	EST_HUMAN	601304181F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2579	15293	28030	1.97	4.0E-03	U52111.2	NT	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2579	15293	28031	1.97	4.0E-03	U52111.2	NT	Homo sapiens X23 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), GDM protein (GDM), adrenoleukodystrophy protein >
2696	15405	28140	3	4.0E-03	AJ277365.1	NT	Homo sapiens X23 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), GDM protein (GDM), adrenoleukodystrophy protein >
2696	15405	28141	3	4.0E-03	AJ277366.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3219	15982	28634	1.16	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
3219	15982	28635	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151:299-003-H08 HT0340 Homo sapiens cDNA
3521	16277	28931	0.87	4.0E-03	AW188426.1	EST_HUMAN	PM1-HT0340-151:299-003-H08 HT0340 Homo sapiens cDNA
							x9804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2965279 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3621	16277	28932	0.97	4.0E-03	AW188426.1	EST_HUMAN	x58f04.x1 NCL_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3612	16365	29006	0.73	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 611 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3609	16859	29300	0.73	4.0E-03	AF080868.1	NT	Mus musculus tumor susceptibility protein 101 (tag101) gene, complete cds
3677	16726		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5057	17776	30363	0.93	4.0E-03	AW103719.1	EST_HUMAN	x683403.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.14 L1 L1 repetitive element;
5114	17832		0.97	4.0E-03	AA772898.1	EST_HUMAN	ae73405.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:969776 3'
5194	18002	30825	1.8	4.0E-03	AF005859.1	NT	Drosophila melanogaster aron2D7 (aron2D7) mRNA, complete cds
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-calinin binding protein mRNA, complete cds
5705	18499	31421	2.48	4.0E-03	P04196	SWISSPROT	(HPRG)
5708	18502	31423	1.74	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZITE ANTIGEN PRECURSOR
5782	18563	31510	0.98	4.0E-03	AL133871.1	EST_HUMAN	DKFp76111014.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFp76111014 5'
5993	18774		4.11	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6140	18918	31868	0.95	4.0E-03	AW560572.1	EST_HUMAN	hg46c07.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2948652 3'
6217	18991	31967	1.8	4.0E-03	BE548463.1	EST_HUMAN	601076015F1 NH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6572	19336	32347	1.28	4.0E-03	AA813222.1	EST_HUMAN	aj32f1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1302045 3'
6677	19594	32632	1.91	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKN3) mRNA, complete cds
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	19787	32851	3.5	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7331	20013	33061	1.23	4.0E-03	AI681483.1	EST_HUMAN	537g12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7333	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	7631b02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7424	20101		0.74	4.0E-03	X92109.1	NT	H. sapiens hcglX gene
7843	20538	33666	0.7	4.0E-03	Q9T192	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS6) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
7847	20942	33767	5.45	4.0E-03	AF111944.1	NT	Dactyloscillus discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8103	20797	33928	2.06	4.0E-03	7662067	NT	Homo sapiens KIA0345 gene product (KIA0345), mRNA
8614	21306	34448	6.98	4.0E-03	AI553983.1	EST_HUMAN	be49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
8787	21479		4.25	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9827	22478	35679	0.67	4.0E-03	H30684.1	EST_HUMAN	yp42g12.r1 Soares_retina_N2b5f.r1 Homo sapiens cDNA clone IMAGE:190150 5'
10275	22923	36135	1.3	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
10466	23112		0.45	4.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11074	23744	37017	4.09	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
11777	24368	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	25385		1.78	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-18300-002-b08 BN0138 Homo sapiens cDNA
12187	24649		2.38	4.0E-03	BE298290.1	EST_HUMAN	601118184F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12246	24694		2.27	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-aj-p-04-Q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	7q74c06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12521	25283		2.08	4.0E-03	AW614596.1	EST_HUMAN	h02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2653932 3' similar to contains element LTR3 repetitive element;
12801	25048	30956	2.17	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0671), mRNA
392	13160	25803	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26299	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA468110.1	EST_HUMAN	nc73c06.s1 NCI_CGAP_Py2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14982		1.38	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2292	15017		6.44	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2293	15018	27753	1.09	3.0E-03	U48858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2293	15018	27754	1.09	3.0E-03	U48858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3081	15846	28488	3.31	3.0E-03	BE379286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609633 5'
3149	15912	28557	2.52	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3412	16170	28819	1.72	3.0E-03	U34603.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3420	16177		5.97	3.0E-03	Y12500.1	NT	C.elegans semd6 gene
3959	16708	29348	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3959	16708	29349	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4016	16762	29390	1.35	3.0E-03	A1792278.1	EST_HUMAN	af04f09.y5 Gesseler Wilms tumor Homo sapiens cDNA clone IMAGE:1155889 5'
4130	16872		1	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4364	17102	29737	5.63	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4428	17164		0.73	3.0E-03	BE348739.1	EST_HUMAN	h08g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4482	17217	29844	4.97	3.0E-03	AF366141.1	EST_HUMAN	xu8.P10.H3 conom Homo sapiens cDNA 3'
4782	17514	30136	2.38	3.0E-03	AF792754.1	EST_HUMAN	ab18a06.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4802	17533	30155	7.94	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5184	17892	30508	3.98	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5468	18267	31159	1.98	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)



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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5539	18337	31244	0.99	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	19225	32225	11.75	3.0E-03	AA458701.1	EST_HUMAN	aa13f10.r1 Soereg_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19782	32857	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pop3 gene for purine-cytosine permease
7422	20089	33187	3.64	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7839	20534	33661	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-251900-032-e07 BT0812 Homo sapiens cDNA
7839	20534	33662	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-251900-032-e07 BT0812 Homo sapiens cDNA
8056	20750	33881	1.54	3.0E-03	N92580.1	EST_HUMAN	z627004.s1 Soereg_parityoid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20808		0.51	3.0E-03	M63498.1	NT	S.cerevisiae UGA36 gene, complete cds
8360	21053	34194	1.32	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8361	21074	34213	1.47	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8485	21177		1.29	3.0E-03	Q9QV81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8890	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	h180710.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2689131 3' similar to contains L1.L1 L1 repetitive element:
8943	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8967	21657	34808	6.44	3.0E-03	A1016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1
8977	21667	34817	0.73	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9309	21976		0.83	3.0E-03	D90801.1	NT	602035880F1 NC_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4183938 5'
9347	20418	33538	0.83	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9536	22189		0.54	3.0E-03	P03365	SWISSPROT	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA
9806	22259		3.88	3.0E-03	P08672	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPORZONTE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
9795	22446	35651	1.3	3.0E-03	P11369	SWISSPROT	ENDONUCLEASE]
9896	22546	35740	1.29	3.0E-03	P51089	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10040	22888	35906	3.97	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10752	23437		1.9	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11137	20099	33187	2.65	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11363	24043	37346	1.89	3.0E-03	AF009222.1	NT	Pneumocystis carinii kdsr-like serine endoprotease mRNA, partial cds
11424	23191	36422	2.52	3.0E-03	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11462	24065	37372	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11462	24065	37373	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.88	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]



Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW294812.1	EST_HUMAN	UI-H-B12-ah1-4-6-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
11927	25198		2.88	3.0E-03	AI525056.1	EST_HUMAN	promina-5.E07.r bvtumor Homo sapiens cDNA 5'
11962	24510	37256	1.88	3.0E-03	AA983154.1	EST_HUMAN	α77b10.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER28 repetitive element;
12016	25321		2.28	3.0E-03	AB008098.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12180	24681	31068	2.71	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for connexin38 (cx38 gene)
502	13288	25019	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15552		12.31	2.0E-03	T70874.1	EST_HUMAN	Yd15h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1342	14090	26768	2.07	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	AA061805.1	EST_HUMAN	nu8801.s1 NCI_CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1217593
1354	14102	26777	18.16	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26906	1.73	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD181 ANTIGEN)
1506	14252	26938	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1586	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1764	14506	27207	1.13	2.0E-03	AA450138.1	EST_HUMAN	zy42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144808.1	EST_HUMAN	CM2-HT0183-061089-018-d03 HT0183 Homo sapiens cDNA
1888	14724	27445	1.57	2.0E-03	AF302801.1	NT	Mus musculus myosin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.18	2.0E-03	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15298		4.57	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adj-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450138.1	EST_HUMAN	zy42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF068855.1	EST_HUMAN	602183800T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3657	16410	28048	6.62	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4093	16835	28461	1.96	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4195	16936		11.03	2.0E-03	U68401.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4393	17130		1.12	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-adj-g-03-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4397	17134	28765	0.97	2.0E-03	AI094746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4508	17244	29877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (sha) mRNA, complete cds
4509	17244	29878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (sha) mRNA, complete cds
4663	17397		1.84	2.0E-03	R87773.1	EST_HUMAN	y045602.s1 Soares adult brain N2b4HB50Y Homo sapiens cDNA clone IMAGE:180890 3'
4956	17682	30290	2.57	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5092	17811	30427	1	2.0E-03	BE798380.1	EST_HUMAN	601583004F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937560 5'
5399	18199	30863	1.38	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104602 5'
5540	25070	31245	2.06	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0863 protein, partial cds
5623	18420	31333	1.86	2.0E-03	U63711.1	NT	Xenopus laevis xanillin mRNA, complete cds
6019	18800	31760	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03	Q98203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6253	19027	32002	2.17	2.0E-03	Q98203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6255	19029	32004	7.5	2.0E-03	BF306187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6291	19064	32046	2.44	2.0E-03	Q9UKP4	SWISSPROT	ADAM-7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19065	32047	0.98	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6320	19090	32078	1.62	2.0E-03	X94451.1	NT	Leuciscutum mRNA for lysyl-tRNA synthetase (LysRS)
6506	19271		1.16	2.0E-03	A1891088.1	EST_HUMAN	wu36h09.x1 Soares_Diedknecht_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 80S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
6541	19306	32311	0.61	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
6862	17939	30575	1.52	2.0E-03	AB038602.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6939	19674	32720	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIc fusion partner (LHFP) mRNA
6939	19674	32721	0.6	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIc fusion partner (LHFP) mRNA
6981	19506	32531	3.55	2.0E-03	BE067988.1	EST_HUMAN	CM4-BT0368-061292-054-d01 BT0368 Homo sapiens cDNA
7044	19735	32795	0.58	2.0E-03	AI298883.1	EST_HUMAN	qm98d11.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1806885 3'
7193	19879	32953	0.8	2.0E-03	T88599.1	EST_HUMAN	y077g10.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7517	20188	33281	1.16	2.0E-03	P07364	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7950	20845	33769	1.96	2.0E-03	AW592004.1	EST_HUMAN	ht37b08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q00976 Q00976 JERRY;
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	y042g08.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1 b2 L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8110	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	y442g06.s1 Soares melanocyte 2NbtHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8162	20856	33987	0.54	2.0E-03	Q82350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C639.05 IN CHROMOSOME 1
8184	20878	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20933	34069	0.81	2.0E-03	6005855	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	34070	0.81	2.0E-03	6005856	NT	Homo sapiens Ratina-derived POU-domain factor-1 (RPF-1), mRNA
8264	20958	34097	0.88	2.0E-03	AU136879.1	EST_HUMAN	AU136879 PLACET1 Homo sapiens cDNA clone PLACE1004839 5'
8318	21011			2.0E-03			Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21282	34400	0.54	2.0E-03	AJ400877.1	NT	Oryctolagus cuniculus mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AB035256.1	NT	MR2-UM0025-303300-102-402 UM0025 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-303300-102-402 UM0025 Homo sapiens cDNA
9139	21827	34992	0.64	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9426	22104	35276	0.89	2.0E-03	H50832.1	EST_HUMAN	y986a09.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194298 3'
9426	22104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	y986a09.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194298 3'
9458	22008	35178	3.46	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENDINOUS: ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9568	22219	35404	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9568	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35484	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9623	22276	35485	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22486	35668	0.81	2.0E-03	AW894269.1	EST_HUMAN	QV3-OT0084-000-100-144-s01 OT0084 Homo sapiens cDNA
9942	22590		5.75	2.0E-03	AA251978.1	EST_HUMAN	za10a08.s1 NCI C-GAP_GCB1 Homo sapiens cDNA clone IMAGE:084754 3'
10506	23152	36377	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141C99-012-d01 CT0251 Homo sapiens cDNA
10506	23152	36378	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141C99-012-d01 CT0251 Homo sapiens cDNA
10938	23618		2.97	2.0E-03	M86524.1	NT	Human dystrophin gene
11470	20188	33281	2.58	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11538	24138	37446	9.1	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
11909	24473		3.23	2.0E-03	AI625745.1	EST_HUMAN	y95h03.x1 NCI C-GAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11926	24487	37807	2.41	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G; Homo sapiens SEL1L (SEL1L) gene, partial cds

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11949	24502	37810	2.41	2.0E-03	A1084325.1	EST_HUMAN	oy43g06.s1 Soares_parityroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 PS-PLA1 PRECURSOR. ;
11972	17907		9.37	2.0E-03	AJ245167.1	NT	Carnelius dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12172	25381		2.99	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
12262	24707	31050	1.76	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12433	25224		1.48	2.0E-03	A1375037.1	EST_HUMAN	hs03002.x1 Soares_tetis_Nb2HF8_0w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element
12542	24882		1.64	2.0E-03	AF129786.1	NT	Homo sapiens MSH55 gene, partial cds; and GLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12713	25175		2.65	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
429	13215	25860	1.28	1.0E-03	H96471.1	EST_HUMAN	y68c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
810	13581	26248	2.31	1.0E-03	A1720263.1	EST_HUMAN	es70b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
810	13581	26249	2.31	1.0E-03	A1720263.1	EST_HUMAN	es70b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1073	13831	26489	3.78	1.0E-03	A1665788.1	EST_HUMAN	w48a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422268 3'
1093	13951	26510	1.78	1.0E-03	A1954572.1	EST_HUMAN	w48a10.x1 NCI_CGAP_Med15 Homo sapiens cDNA clone IMAGE:2551242 3'
2021	14758	27486	3.38	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2160	14880	27614	12.13	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2979	15745	28393	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3186	15949	28599	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3186	15949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3656	16409		1.65	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4402	17139	28767	1.28	1.0E-03	BE839162.1	EST_HUMAN	RC1-TN0128-180300-021-g01 TN0128 Homo sapiens cDNA
4441	17177	28803	4.05	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4009 Proliferic pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4009
4616	17350	29686	0.84	1.0E-03	U29446.1	NT	Cenorchaditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL6) genes
4773	17505	30127	1.68	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4773	17505	30128	1.68	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4774	17506		4.29	1.0E-03	BE164067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5018	17739	30348	7.24	1.0E-03	O49409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5225	18032	30958	1.87	1.0E-03	AA280851.1	EST_HUMAN	zs44f01.r1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AJ006345.1	NT	Homo sapiens K/LQT1 gene
5369	18170	30858	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5369	18170	30857	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5485	18284	31182	0.83	1.0E-03	BE798491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5491	18280	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5546	18343	31251	0.67	1.0E-03	N41874.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41874.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5930	18714		2.75	1.0E-03	X07899.1	NT	Mouse nucleolin gene
5988	18750	31711	1.07	1.0E-03	BE963939.2	EST_HUMAN	601667519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875893 3'
6099	18877		8.78	1.0E-03	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6242	19018	31990	1.14	1.0E-03	T87781.1	EST_HUMAN	y03a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6315	19086		1.7	1.0E-03	AW802585.1	EST_HUMAN	QV3-NN1024-280400-171-q05 NN1024 Homo sapiens cDNA
6657	19418	32432	1.37	1.0E-03	L77570.1	NT	Homo sapiens D1George syndrome critical region, centromeric end
7052	19743	32805	2.54	1.0E-03	D18828.1	NT	Human gene for fourth semaphorin receptor subtype
7639	20209	33308	1.8	1.0E-03	U52111.2	NT	Homo sapiens X28i region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM1), adrenoleukodystrophy protein >
7608	20274	33382	3.37	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7656	20320	33429	0.98	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3893278 5'
7789	20484	33608	0.83	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7850	20545	33673	5.18	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8043	20737	33870	1	1.0E-03	AA122270.1	EST_HUMAN	zh07c09.s1 Soares_pregnant_uterus_NH-IPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element;
8142	20836	33968	1.94	1.0E-03	AF153980.1	NT	Homo sapiens excise-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8329	21022	34158	0.68	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8492	21184	34326	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8842	21534		1.36	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxpsin
8869	21580	34705	0.62	1.0E-03	AW840363.1	EST_HUMAN	CM8-LT0079-170210-092-e07 LT0079 Homo sapiens cDNA

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		0.58	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34858	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cti subunit mRNA, complete cds
9017	21707	34859	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cti subunit mRNA, complete cds
9507	22160	35340	1.66	1.0E-03	AF011400.1	NT	Thermoboga neocitara alpha-1,6-galactosidase (aglA) gene, complete cds
9507	22160	35341	1.66	1.0E-03	AF011400.1	NT	Thermoboga neocitara alpha-1,6-galactosidase (aglA) gene, complete cds
9720	22371	35570	0.81	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10063	22711	35929	0.65	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10068	22716		0.75	1.0E-03	AF067485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10214	22862	36075	1.72	1.0E-03	A1024350.1	EST_HUMAN	ov7508.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element;
10503	23149		0.46	1.0E-03	AA706202.1	EST_HUMAN	ag93f12.a1 Strategene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element
10563	23259	36495	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-18:099-011-409 CT0279 Homo sapiens cDNA
10563	23259	36496	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-18:099-011-409 CT0279 Homo sapiens cDNA
10651	23342	36580	2.78	1.0E-03	BE170659.1	EST_HUMAN	QV3-HT0543-220300-130-403 HT0543 Homo sapiens cDNA
10726	23413		3.29	1.0E-03	A1583847.1	EST_HUMAN	W73a12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248448 3' similar to TR:Q28195 Q28195 PVA1 GENE.;
10908	23491	36727	1.36	1.0E-03	AW237482.1	EST_HUMAN	xm72d12.x1 NCI_CGAP_K4111 Homo sapiens cDNA clone IMAGE:2689751 3'
11106	23776		3.05	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11806	24470	37806	4.48	1.0E-03	BE804488.1	EST_HUMAN	607433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3978524 6'
12124	24616		1.38	1.0E-03	AV731520.1	EST_HUMAN	AV731520 HTF Homo sapiens cDNA clone HTFAJG05 5'
12371	25342		1.98	1.0E-03	A1347355.1	EST_HUMAN	ts05h11.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12478	25365	30612	7.05	1.0E-03	BE780572.1	EST_HUMAN	607468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
12821	25187	30808	1.37	1.0E-03	AW847341.1	EST_HUMAN	RCO-CT0205-240388-021-402 CT0205 Homo sapiens cDNA
5130	17848	30465	0.7	9.0E-04	P06548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5598	18391		1.28	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6165	18942		0.6	9.0E-04	AJ006345.1	NT	Homo sapiens Kv1.2T1 gene
6395	19164	32165	0.96	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9543	22196		1.42	9.0E-04	AB037203.1	NT	Glycylthia glabra GgBAS1 mRNA for beta-amylin synthase, complete cds
1471	14218		1.02	8.0E-04	X90469.1	NT	Xlaevis mRNA for C4SR protein

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4159	16899		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U20185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.93	8.0E-04	AA77084.1	EST_HUMAN	z124c10.s1 Soares fetal_NBHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11206	23928		1.98	8.0E-04	A1571099.1	EST_HUMAN	tr85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119	27866	0.87	7.0E-04	U20185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	15426	28164	1.19	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3274	16035	28685	1	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6005	18786	31748	0.94	7.0E-04	AA516212.1	EST_HUMAN	ngd5g12.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1 b3 L1 L1
6420	19188		2.47	7.0E-04	A1768331.1	EST_HUMAN	repetitive element;
7128	19816		0.78	7.0E-04	AK024445.1	NT	wg30f09.x1 Soares NSF F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
9703	22354	35549	0.53	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00355 protein, partial cds
9703	22354	35550	0.53	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24156		2.28	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11686	24185	37500	4.04	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12642	24939		2.31	7.0E-04	R17336.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:232288 5'
12688	24964		5.98	7.0E-04	6005855	NT	yg13c06.j1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2402878 3'
3941	16891	29329	1.83	6.0E-04	A1862525.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4068	16812	29440	0.78	6.0E-04	K01315.1	NT	w15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4068	16812	29441	0.78	6.0E-04	K01315.1	NT	Homo sapiens epistatin-1 pseudogene (IGHEP1) gene, 5' flanking region
4162	16802	29531	3.70	6.0E-04	U45983.1	NT	Homo sapiens epistatin-1 pseudogene (IGHEP1) gene, 5' flanking region
7478	20181	33245	0.81	6.0E-04	Q15034	SWISSPROT	Homo sapiens GCR8 chemokine receptor (CMKBR8) gene, complete cds
7765	20461		3.33	6.0E-04	P46408	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7914	20609		0.62	6.0E-04	H82947.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 6, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
9880	22530		3.5	6.0E-04	ALD48507.2	EST_HUMAN	y64a11.s1 Soares_joined_gland_N3HPG Homo sapiens cDNA clone IMAGE:231958 3' similar to contains LOR1 repetitive element;
9980	22628	35837	2.26	6.0E-04	BE005850.1	EST_HUMAN	DKFZp586M2024 t1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024
10238	22886		0.71	6.0E-04	AF267478.1	NT	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
11467	24070	37378	2.53	6.0E-04	AJ228042.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM6) mRNA, complete cds
11558	24157	37467	3.46	6.0E-04	AW013847.1	EST_HUMAN	Homo sapiens 559 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11636	24233		2.17	6.0E-04	Q01768	SWISSPROT	UHH-B10-ab-e-09-UJI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708826 3'
12082	25249		2.81	6.0E-04	AW380619.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
							RC1-HT0269-281169-012-408 HT0269 Homo sapiens cDNA



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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12816	25058		1.34	8.0E-04	AI817088.1	EST_HUMAN	wf76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
638	13415	26051	8.81	5.0E-04	OT0341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)
1490	14237		1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-407 CT0225 Homo sapiens cDNA
3408	18186	28815	1.35	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.x1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3704	18457	29096	2.32	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6386	18188	30877	2.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6632	19268	32303	7.89	5.0E-04	AA158080.1	EST_HUMAN	z033b08.r1 Striatogene colon (#337204) Homo sapiens cDNA clone IMAGE:588663 5'
7276	19960	33037	3.75	5.0E-04	M23804.1	NT	Gorilla gorilla Invictin gene medium allele, complete cds
7856	20551	33077	5.2	5.0E-04	AI188382.1	EST_HUMAN	qdt13f08.x1 Soares_placenta_9to6weeks_2NlRP8t69W Homo sapiens cDNA clone IMAGE:172819 3' similar to gb:X51002_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
8202	20906	34033	0.96	5.0E-04	AA814519.1	EST_HUMAN	cb06a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9177	21847	35013	1.39	5.0E-04	AA846545.1	EST_HUMAN	q156h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9271	22025	35195	0.68	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9418	22096	35288	1.44	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
9508	22162	35344	4.1	5.0E-04	AW270888.1	EST_HUMAN	xs06a02.x1 NCI_CGAP_Kdt11 Homo sapiens cDNA clone IMAGE:2768858 3'
10177	22825		0.49	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
10807	23577		2.38	5.0E-04	AL048607.2	EST_HUMAN	DKFZp686M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp686M2024
11713	18186	30877	14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12020	25184		5.04	5.0E-04	AA569513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:913875
658	13435	26076	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26267	1.79	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 ALU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
827	13597	26268	1.79	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 ALU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1449	14198	26880	3.18	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2075	14807	27538	1.81	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2129	14960		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D059 5'
2633	15345	28068	2.21	4.0E-04	O96615	SWISSPROT	SERGIN-2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.95	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	29653	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4289	17028	29654	3.18	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4500	17236	29668	1.78	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Striagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5028	17748	30360	3.1	4.0E-04	BE560660.1	EST_HUMAN	601345895F-1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7168	19655	32925	1.3	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	AL101566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7618	20284	33304	0.58	4.0E-04	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8434	21127	34284	1.07	4.0E-04	BF240712.1	EST_HUMAN	601876885F-1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5'
8442	21134	34270	1.5	4.0E-04	N25607.1	EST_HUMAN	y439a12.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:264142 5'
9590	22243	35428	3.24	4.0E-04	A025699.1	EST_HUMAN	ov67h03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1844341 3'
9740	22391		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12380	25157		2.05	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
152	12967	25808	3.48	3.0E-04	AL119428.1	EST_HUMAN	DKFZp761J221_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
190	13003	25844	2.24	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
860	13629	26300	1.32	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1831	14570	27282	1.08	3.0E-04	A1262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028197 5'
1846	14584		1.21	3.0E-04	A1399674.1	EST_HUMAN	th23a02.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2119082 3'
3303	16064	28712	3.43	3.0E-04	P25147	SWISSPROT	INTERALIN B PRECURSOR
3308	16068	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	z65a04.r1 Soares fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448478 5'
3946	16996	29335	4.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779		1.33	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4072	16816		1.12	3.0E-04	BE140806.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
4766	17498		4.72	3.0E-04	BE163778.1	EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4827	17558	30180	0.95	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221288-046-d08 DT0045 Homo sapiens cDNA
5063	17782	30399	0.96	3.0E-04	AA613145.1	EST_HUMAN	np08g08.s1 NCI_CGAP_Lut1 Homo sapiens cDNA clone IMAGE:1143328 3'
6062	18832		7.86	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6722	19556	32586	2.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7491	20163	33256	0.84	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20851	33983	3.23	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	z48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M82762
10078	22726	35943	0.65	3.0E-04	AI992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 10 KD PROTEOLIPID SUBUNIT (HUMAN);
10358	23003	36220	3.73	3.0E-04	AA781201.1	EST_HUMAN	wf75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10465	23141	36367	0.54	3.0E-04	P13616	EST_HUMAN	424g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
11555	24154	37466	1.38	3.0E-04	4501960	SWISSPROT	RIBOSOMAL PROTEIN L7A (HUMAN);
11976	25386	30817	4.81	3.0E-04	AA228301.1	EST_HUMAN	GLUTAMIC ACID-RICH PROTEIN PRECURSOR
12336	25230	30818	3.08	3.0E-04	AB018292.1	NT	Homo sapiens adrenic, alpha -1A-, receptor (ADRA1A), mRNA
12730	25000		2.75	3.0E-04	AL134483.1	EST_HUMAN	nc38a04.r1 NCL_C3AP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
171	12984	25924	2.95	2.0E-04	AF217796.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
466	13251	25892	1.8	2.0E-04	AU145707.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: mbr1) Homo sapiens cDNA clone DKFZp547L185 5'
887	13656	26324	10.71	2.0E-04	M86524.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein N1L, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
887	13656	26325	10.71	2.0E-04	M86524.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
1156	13911		3.93	2.0E-04	AI289021.1	EST_HUMAN	Human dystrophin gene
1163	13917		2.18	2.0E-04	AL163203.2	NT	Human dystrophin gene
1824	14563		1.12	2.0E-04	AF224268.1	NT	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2581	15295	28033	4.47	2.0E-04	U68061.1	NT	Homo sapiens chromosome 21 segment HS21C003
2986	15752	28398	1.11	2.0E-04	AI124529.1	EST_HUMAN	Mus musculus 5' flanking region of Pib3 gene
3328	16068	28740	1.1	2.0E-04	5174736	NT	Human gemline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
3429	16186	28834	1.99	2.0E-04	BE082317.1	EST_HUMAN	em58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3892	16642	29282	0.79	2.0E-04	AW978441.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
4122	16964		4.93	2.0E-04	U01029.1	NT	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
4620	17355	29990	1.74	2.0E-04	H96265.1	EST_HUMAN	EST390550 MAGP neosequence, MAGP Homo sapiens cDNA
4620	17355	29991	1.74	2.0E-04	H96265.1	EST_HUMAN	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4742	17474		1.63	2.0E-04	U09228.1	NT	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4996	17721	30324	1.1	2.0E-04	AB037897.1	NT	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
							Galus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
							Danio rerio hageroma gene, exons 1 to 6, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5099	17808	30424	1.04	2.0E-04	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMHHC)
5457	18258	31148	0.73	2.0E-04	AV854352.1	EST_HUMAN	AV854352 GLCH Homo sapiens cDNA clone GLCDU10 3'
5499	18268	31180	1.75	2.0E-04	A1800862.1	EST_HUMAN	lq3b11.1x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709 3'
5664	18459	31373	0.86	2.0E-04	AA298852.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
5857	18844	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6144	18922	31892	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	19818		2.6	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7225	19910		0.55	2.0E-04	AW800963.1	EST_HUMAN	QV0-CT0387-18300-167-810 CT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33295	1.42	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.08	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33676	1.08	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20876	34012	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20876	34013	1.23	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8463	21155	34298	1.96	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
8842	21334	34478	0.49	2.0E-04	X57331.1	NT	Human Immunoglobulin G(mu) and C(delta) heavy chain genes (constant regions)
8233	21812	35088	0.49	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9319	21966	35158	0.6	2.0E-04	P18716	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOGF28.1
9875	22526	35719	1.19	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-905 HT0254 Homo sapiens cDNA
9916	22585	35781	1.77	2.0E-04	AA405777.1	EST_HUMAN	zu86c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864 5'
10755	23440	36884	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11128	23798		1.61	2.0E-04	AJ243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
11276	23937	37229	3.06	2.0E-04	AA440282.1	EST_HUMAN	g011f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11403	24052	37356	2.86	2.0E-04	AW136740.1	EST_HUMAN	UI-H-B11-efm-e-04-JUI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
11857	24441	37782	2.77	2.0E-04	AI821304.1	EST_HUMAN	y679b10.x5 Stratagene ovary (#637217) Homo sapiens cDNA clone IMAGE:77371 3'
1053	13812	28472	3.3	1.0E-04	P11399	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1092	13860	28508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-00-JUI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1092	13850	28509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-08-JUI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	AB046342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
3278	19039	28689	1.08	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN Q2 (SAP Q2) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A06)
3719	18472	29110	0.91	1.0E-04	A1440282.1	EST_HUMAN	Human alpha 1 type IV collagen mRNA
4037	18782	29412	2.11	1.0E-04	M14042.1	NT	Mouse alpha 1 type IV collagen mRNA
4062	18807	29437	1.15	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC8B004 3'
5036	17755	30368	1.28	1.0E-04	7062015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7062015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31558	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
5834	18623	31557	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02a12.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:252
6738	19672	32605	0.92	1.0E-04	AA564561.1	EST_HUMAN	rt25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:983486 3' similar to gb:M07252
7098	19776	32841	15.8	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7470	19778	32841	17.82	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
7894	20589	33719	0.95	1.0E-04	AA630453.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
9236	21915	35088	2.27	1.0E-04	A1806220.1	EST_HUMAN	ab94q08.s1 Stratigene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9247	21928	35097	1.46	1.0E-04	O89899	SWISSPROT	wf28a08.x1 Spores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9325	21992		0.49	1.0E-04	T77163.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9546	22189	35381	1.86	1.0E-04	10863876	NT	y172c08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:113774 5'
10079	22727		2.74	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04	M28587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11567	24166	37479	2.05	1.0E-04	AW205336.1	EST_HUMAN	Mouse alpha leukocyte interferon gene, complete cds
11567	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	UI-HB11-sew-a-02-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11649	24246	37586	1.78	1.0E-04	AB032868.1	NT	UI-HB11-sew-a-02-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
							Homo sapiens mRNA for KIAA1142 protein, partial cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11892	24287	37609	2.01	1.0E-04	AW269061.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11725	24319	37643	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11725	24319	37644	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE876398.1	EST_HUMAN	729a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1 repetitive element;
682	13457	26102	2.78	9.0E-05	AA718933.1	EST_HUMAN	ah45ct11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1282468 3'
1997	14733	27455	1.14	9.0E-05	AW868218.1	EST_HUMAN	QV4-SN0023-070400-168-b04 SN0023 Homo sapiens cDNA
5873	18660	31601	1.81	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33242	0.6	9.0E-05	AW204938.1	EST_HUMAN	UHH-B11-ear-d-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7476	20149	33243	0.8	9.0E-05	AW204938.1	EST_HUMAN	UHH-B11-ear-d-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9378	21851		3.02	9.0E-05	D85006.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
9378	21853	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens methyl-OpG binding protein 1 (MBD1) gene, exon 15b
11082	23752	37027	2.68	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11207	23870	37156	1.75	9.0E-05	AB287878.1	EST_HUMAN	q23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
11617	18660	31601	3.5	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12178	26269		6.83	9.0E-05	AF128758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
802	13574	26237	1.97	8.0E-05	AJ251646.1	NT	Plasmodium falciparum mRNA for beta-1,3 glucanase (gnc2 gene)
844	13614		2.75	8.0E-05	AJ251646.1	NT	Plasmodium falciparum mRNA for beta-1,3 glucanase (gnc2 gene)
2850	16716		0.73	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4448	17184	29608	0.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
11099	23769	37045	1.84	8.0E-05	M89197.1	NT	Human hepatoblastin and hepatoblastin-related protein (HP and HPR) genes, complete cds
12765	25242		4.66	8.0E-05	AA279333.1	EST_HUMAN	za88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704553 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
337	13138	25773	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220599-011-E04 CT0208 Homo sapiens cDNA
337	13138	25774	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220599-011-E04 CT0208 Homo sapiens cDNA
554	13337	25965	1.1	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
554	13337	25966	1.1	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1033	13793	28453	1.4	7.0E-05	Q22946	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2724	15431	28168	2.99	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3156	15919	28565	5.72	7.0E-05	AB009080.1	NT	Dicystostellum discoidium gene for TRFA, complete cds
4339	17078	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17149	29776	0.95	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
4871	17598	30221	0.71	7.0E-05	9845300	NT	Rat cytomegalovirus Mestrict1, complete genome
8124	20818	33954	1.09	7.0E-05	AA505582.1	EST_HUMAN	nt83g01.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:988008 3'
9453	22003	35175	2.97	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Striatum, Striatum (cat#936206) Homo sapiens cDNA clone HFBED60
11112	23782		3.09	7.0E-05	10835040	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2020	14755	27484	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	14755	27485	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2595	15309	28046	1.19	6.0E-05	AI655241.1	EST_HUMAN	w654h06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA
2690	15399	28137	1.1	6.0E-05	Z84506.1	NT	TOPOISOMERASE I (HUMAN);
2690	15399	28138	1.1	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
2817	13440	26080	3.07	6.0E-05	AF053690.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA28B10
5822	18611	31541	3.61	6.0E-05	Q12860	SWISSPROT	Homo sapiens myocyte/hematopoietic elastase inhibitor gene, complete cds
5822	18611	31542	3.61	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6309	19081	32066	1.4	6.0E-05	N72829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6834	19496	32520	0.95	6.0E-05	AA697880.1	EST_HUMAN	y50gt11.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7883	20678	33803	0.76	6.0E-05	BE064410.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
7883	20678	33804	0.76	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-H06 BT0311 Homo sapiens cDNA
8342	21035	34172	0.62	6.0E-05	AA150482.1	EST_HUMAN	RC4-BT0311-141198-011-H06 BT0311 Homo sapiens cDNA
8347	21040	34177	2.22	6.0E-05	AW896629.1	EST_HUMAN	Z08c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to
8479	21171	34316	0.63	6.0E-05	Q00401	SWISSPROT	contains element MER28 repetitive element;
9151	21882	35050	1.21	6.0E-05	P08607	SWISSPROT	PM4-NN0050-310300-001-F10 NN0050 Homo sapiens cDNA
9151	21882	35051	1.21	6.0E-05	P08607	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9421	22099	35271	0.85	6.0E-05	T94149.1	EST_HUMAN	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9621	22274	35462	0.59	6.0E-05	AW627985.1	EST_HUMAN	C4B-BINDING PROTEIN PRECURSOR (C4BP)
10649	23340	36579	3.06	6.0E-05	R75639.1	EST_HUMAN	y528c12.t1 Striatum lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
11502	24103	37415	3.36	6.0E-05	AA044015.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:297444 3'
12887	25239	30822	14.34	6.0E-05	AW890110.1	EST_HUMAN	y59d08.s1 Soares placenta Nb2IP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu
12810	25053		1.4	6.0E-05	BE58403.1	EST_HUMAN	repetitive element; contains LTR7 repetitive element;
1392	14129	26802	10.46	5.0E-05	AW392086.1	EST_HUMAN	z658f02.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1855	14593		1.2	5.0E-05	8923891	NT	Homo sapiens 2.6kDa peroxisomal membrane protein-like (LOC55895), mRNA
2551	15206	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3061	16710	28350	2.41	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17793	30408	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17793	30409	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X58855.1	NT	Human MLC1 gene for embryonic myosin alkaline light chain, 3' UTR
5903	18688	31638	3.75	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC1 Homo sapiens cDNA clone GLODMA06 3'
6076	18855	31822	0.99	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19016		0.87	5.0E-05	AB037064.1	NT	Mus musculus gene for calretinin, exon 1
12176	24810		3.64	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4449	17185	29809	0.73	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	29810	0.73	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
6841	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9423	22101		7.57	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9901	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10306	22953	36168	0.59	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10668	23359	36590	4.18	4.0E-05	AW027946.1	EST_HUMAN	h38c07.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
12140	24029		1.48	4.0E-05	AW117580.1	EST_HUMAN	element MIR repetitive element;
12789	25041		1.71	4.0E-05	AA417766.1	EST_HUMAN	xd53e08.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
695	13441	28062	1.6	3.0E-05	A1248061.1	EST_HUMAN	z01et11.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
1037	13797	28457	0.86	3.0E-05	AW279851.1	EST_HUMAN	q04c10.x1 Scores: fetal_liver_apical_NFL_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1109	13868	26523	1.01	3.0E-05	BF037898.1	EST_HUMAN	x24g03.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1109	13868	26524	1.01	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
3287	18048		0.73	3.0E-05	A1288919.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
4349	17088	29719	7.98	3.0E-05	BE169211.1	EST_HUMAN	q01g11.x1 Scores: NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:008632
4349	17088	29720	7.98	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120:300-001-010 HT0521 Homo sapiens cDNA
							PM1-HT0521-120:300-001-010 HT0521 Homo sapiens cDNA



Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	29788	0.94	3.0E-05	AA368679.1	EST_HUMAN	EST78996 Placenta   Homo sapiens cDNA similar to similar to p53-associated protein
4434	17170	29789	0.94	3.0E-05	AA368679.1	EST_HUMAN	EST78996 Placenta   Homo sapiens cDNA similar to similar to p53-associated protein
4550	17285		0.99	3.0E-05	AL169302.2	NT	Homo sapiens chromosome 21 segment HS21G102
4698	17420	30055	1	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	28082	0.82	3.0E-05	A1248061.1	EST_HUMAN	chr4c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
4791	17522	30144	0.97	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002075 5'
5470	18269	31161	1.66	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6659	19419	32433	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6659	19419	32434	1.17	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7799	20404	33616	2.33	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8250	20844	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	zs60p05.s1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8791	21483	34630	1.58	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:3006638 3'
8795	21487	34633	1.23	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8799	21491	34638	0.51	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9029	21719		0.56	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21899	35086	1.22	3.0E-05	AA372662.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' and
9563	22216		2.92	3.0E-05	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
10433	23079	36303	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24585		1.77	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2323	15048	27784	1.09	2.0E-05	A1286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15301	28037	2.43	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element;
						NT	Human adenosine deaminase (ADA) gene, complete cds
2718	15425		7.45	2.0E-05	AA180562.1	EST_HUMAN	zq46a12.r1 Stratigene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
3134	15899	28544	1.23	2.0E-05	BE068036.1	EST_HUMAN	contains Alu repetitive element; contains element L1 repetitive element;
3343	16102	28754	0.93	2.0E-05	AF184614.1	NT	RC3-BT0319-120:200-014-108 BT0319 Homo sapiens cDNA
3362	16121	28779	1.22	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3486	16242		0.71	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3787	16539		0.78	2.0E-05	AL039107.1	EST_HUMAN	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4643	17377		1.09	2.0E-05	BE378471.1	EST_HUMAN	DKFZp5681064_r1 568 (synonym: hfd2) Homo sapiens cDNA clone DKFZp5681064 5'
5672	18467	31392	1.92	2.0E-05	AJ011712.1	NT	601298455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
						NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)



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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18616		0.69	2.0E-05	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
5880	18686	31608	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
5880	18686	31607	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6065	18844	31808	0.61	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_plecenta_8to9weeks_2NhtHP8ta9W Homo sapiens cDNA clone IMAGE:1715114 3'
6527	19293	32297	2.28	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
6801	19462	32483	3.27	2.0E-05	Y08928.1	NT	hw06d12.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6814	19476	32497	1.12	2.0E-05	A1492880.1	EST_HUMAN	P. falciparum mRNA for AAP1 protein, partial
6824	19485		9.37	2.0E-05	A1991025.1	EST_HUMAN	q247008.x1 NCI CGAP_Kht11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
7053	19744	32806	1.93	2.0E-05	AF224282.1	NT	O02711 PRO-POL-OUTPASE POLYPROTEIN; wu35h07.x1 Soares_Dieckgreffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
7053	19744	32807	1.93	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7267	19851		0.83	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7785	20480	33605	1.71	2.0E-05	A1381040.1	EST_HUMAN	Homo sapiens trichostema N-methyltransferase (NMT) mRNA, NMT-2 allele, complete cds
9020	21710	34962	0.53	2.0E-05	BE244840.1	EST_HUMAN	ig20h05.x1 NCI CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2109369 3'
9020	21710	34963	0.53	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1690 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35002	0.58	2.0E-05	P49457	SWISSPROT	TCBAP2E1690 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35003	0.58	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9823	22474	35677	0.49	2.0E-05	A1163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10035	22683	35800	0.87	2.0E-05	BF055939.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10457	23103	36333	0.54	2.0E-05	A1131024.1	NT	717508.y1 NCI CGAP_Brm20 Homo sapiens cDNA clone IMAGE:3340578 5'
10457	23103	36334	0.54	2.0E-05	A1131024.1	NT	Homo sapiens class gene, exon 1-alpha
10489	23135	36382	1.98	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens class gene, exon 1-alpha
10489	23135	36382	1.98	2.0E-05	N41751.1	EST_HUMAN	hw91a06.r1 Soares_plecenta_8to9weeks_2NhtHP8ta9W Homo sapiens cDNA clone IMAGE:259570 5'

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10489	23135	36363	1.98	2.0E-05	N41751.1	EST_HUMAN	yw91a03.r1 Soares_placenta_8to8weeks_2Nb1P8b9W Homo sapiens cDNA clone IMAGE:256970 5'
10541	19485		2.42	2.0E-05	A1991025.1	EST_HUMAN	wu35b07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11287	23948	37243	1.33	2.0E-05	A1453285.1	EST_HUMAN	tt30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.;
11287	23948	37244	1.33	2.0E-05	A1453285.1	EST_HUMAN	tt30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.;
11430	23197	36428	2.27	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-28300-012-E12 HT0582 Homo sapiens cDNA
12185	25168		4.86	2.0E-05	BE348228.1	EST_HUMAN	hw21a03.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12632
12342	25155		2.27	2.0E-05	AF275948.1	NT	Q12832 GLYCOPHORIN HEP2;
12674	25247		1.44	2.0E-05	D16583.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2285	14691	27731	3.22	1.0E-05	P27446	SWISSPROT	Human gene for L-histidine decarboxylase, complete cds
2700	15003	28143	1.6	1.0E-05	AL163282.2	NT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
3641	16394	29034	1.91	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3793	16545		1.02	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Lembo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3949	16989	29337	9.2	1.0E-05	P81274	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4152	18904	29523	1.2	1.0E-05	AL163203.2	NT	MOSAIC PROTEIN LGN
4244	18985	29608	2.52	1.0E-05	AA431119.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4799	17530	30152	1.81	1.0E-05	AW419134.1	EST_HUMAN	zw98g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
6653	19415	32428	1.22	1.0E-05	AJ246003.1	NT	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2858548 3'
6980	19505	32530					Homo sapiens Spast gene for spastin protein
6982	19575	32722	2.58	1.0E-05	AA041846.1	EST_HUMAN	ns19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element;
7677	20341		1.16	1.0E-05	P19474	SWISSPROT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8813	21505		2.24	1.0E-05	AL163227.2	NT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8958	21649	34790	3.02	1.0E-05	AA452578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9167	21657	35022	12.45	1.0E-05	AA236110.1	EST_HUMAN	zq35h12.s1 Soares_testis_Nb2HF8 Sw Homo sapiens cDNA clone IMAGE:788519 3' similar to gb1L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9296	22020	35189	0.62	1.0E-05	AV732190.1	EST_HUMAN	zs05a11.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
9798	22389	35593	0.74	1.0E-05	AW510802.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
							hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element;

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	22389	36594	0.74	1.0E-05	AW510902.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
9816	22467	36669	1.16	1.0E-05	AW291521.1	EST_HUMAN	OFR11 OFR repetitive element;
9816	22467	36670	1.16	1.0E-05	AW291521.1	EST_HUMAN	U1H-B12-egk-e-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW466995.1	EST_HUMAN	U1H-B12-egk-e-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							h407c10.x1 NCI_CGAP_Kdrl2 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1:12 L1 repetitive element;
10636	23518	36780	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, FoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10636	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, FoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11864	24438	37780	1.38	1.0E-05	AF111107.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfoe gene, complete cds; and unknown gene
2678	15387	28129	4.8	9.0E-06	AI683811.1	EST_HUMAN	h73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3092	15857	28498	3.53	9.0E-06	AI218983.1	EST_HUMAN	cg11b08.x1 Soares_placenta_8to8week_2NkHP8b9W Homo sapiens cDNA clone IMAGE:1759191 3'
3597	18350		2.82	9.0E-06	MB1755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5815	18604	31532	2.81	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6785	19509	32534	0.8	9.0E-06	BE069042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7340	20021	33099	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7673	20337	33450	13.94	9.0E-06	AI034370.1	EST_HUMAN	ca20g01.x1 Sodius_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1668912 3' similar to contains Alu repetitive element;
8363	21056	34197	1.1	9.0E-06	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
8881	21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8881	21572	34716	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9122	21810	34976	4.3	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10858	23538	36784	3.46	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2532	15567	27986	1.27	8.0E-06	AW362539.1	EST_HUMAN	RC3-C10283-201189-011-111 CT0283 Homo sapiens cDNA
10430	23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASIGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36289	0.75	8.0E-06	P34083	SWISSPROT	FASIGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
958	13723		2.68	7.0E-06	AA066728.1	EST_HUMAN	ab00f10.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1419	14167	26851	3.42	7.0E-06	7682177	NT	MER20.t1 MER20 repetitive element ;
2876	15943		5.93	7.0E-06	A1368252.1	EST_HUMAN	qiv18g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3551	16306		0.92	7.0E-06	AA385542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5609	18405		5.68	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-251400-173-h01 OT0062 Homo sapiens cDNA
5715	18508	31429	1.01	7.0E-06	N88645.1	EST_HUMAN	yv65c07.r1 Scores_multiple_sclerol_2Nbl-MSP Homo sapiens cDNA clone IMAGE:278412 5'
8888	21380	34524	0.7	7.0E-06	11420708	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF88S1E), mRNA
8800	22451		0.45	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	25356	30608	2.32	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2018	15884	28329	1.28	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-01C300-105-d11 BT0379 Homo sapiens cDNA
3680	16433	23076	1.08	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0379-01C300-105-d11 BT0379 Homo sapiens cDNA
4705	15708	28359	1.91	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4710	17442	30074	2.21	6.0E-06	A1040099.1	EST_HUMAN	cd08e02.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ;
5285	18071	30700	1.32	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9766	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	IL6-UM0070-110-00-063-p02 UM0070 Homo sapiens cDNA
12755	25016	30979	2.27	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5970	18752	31713	3.27	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6245	18019	31993	2.31	5.0E-06	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8804 Met protein (M8804 Met) gene, complete cds
7134	19821	32887	1.1	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8359	21052	34192	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8359	21052	34193	0.53	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10002	22650	35882	6.16	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Odon: ceratonia (HCC) cell line Homo sapiens cDNA 5' end
10410	23056	36273	0.45	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12849	24953	30987	2.83	5.0E-06	A1095045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
632	13411	28046	6.1	4.0E-06	R16287.1	EST_HUMAN	ya48c03.r1 Scores: Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
826	13596	26266	7.07	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eco2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1311	14059	26733	4.64	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1311	14059	26734	4.64	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1457	14204	26889	1.8	4.0E-06	BF366612.1	EST_HUMAN	QV2-NT0046-200600-250-107 NT0046 Homo sapiens cDNA
2261	14988	27728	2.17	4.0E-06	AW015401.1	EST_HUMAN	UIH-B10-ast-f05-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3060	13826	28471	0.9	4.0E-06	AF198349.1	NT	Gallus gallus Dactyl2 protein (Dact2) mRNA, complete cds
3874	16624	29262	1.05	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150:200-074-B03 CT0214 Homo sapiens cDNA
4756	17488	30115	1.89	4.0E-06	A1888039.1	EST_HUMAN	wf94c10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8397	21090	34225	0.56	4.0E-06	O16393	SWISSPROT	MER22 repetitive element;
8699	21391	34536	3.56	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9607	22280	35446	1.24	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11427	23194	36425	4.21	4.0E-06	AB007665.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2160	14990	27624	1.75	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0468
2160	14990	27625	1.75	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
2283	14989		1.44	3.0E-06	AF202635.1	NT	contains L1.11 L1 repetitive element;
2922	15988	28332	1.05	3.0E-06	AA868218.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
3259	18021		2.05	3.0E-06	A1857779.1	EST_HUMAN	contains L1.11 L1 repetitive element;
3763	18515	29152	1.13	3.0E-06	BE047094.1	EST_HUMAN	Homo sapiens PF1200 mRNA, complete cds
3763	18515	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
4524	17259	28893	3.74	3.0E-06	X54816.1	NT	LTR1 repetitive element;
6068	18847	31811	0.93	3.0E-06	AU159412.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
7129	19817		2.43	3.0E-06	P08548	SWISSPROT	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
7981	20676	33801	0.83	3.0E-06	BE62964.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
8584	21276	34413	0.68	3.0E-06	P07743	SWISSPROT	h964d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
12349	24755		3.84	3.0E-06	AW395262.1	EST_HUMAN	h964d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
197	13010		2.81	2.0E-06	P54366	SWISSPROT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
1661	14308		4.45	2.0E-06	P21414	SWISSPROT	terminus.)
2376	15096	27838	4.8	2.0E-06	A1672138.1	EST_HUMAN	terminalus.)

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Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2469	15187	27928	2.37	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	15285	28023	1.88	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16285	28919	1.12	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3744	16497	29132	1.59	2.0E-06	AA173518.1	EST_HUMAN	z002805.t1 Stratigene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:595232 5'
3753	16505	29141	0.82	2.0E-06	AW450215.1	EST_HUMAN	UI-H-B13-aky-g-05-UJ.s1 NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3758	16510	29146	1.82	2.0E-06	AB030898.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5998	18779		0.83	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558809 3' similar to contains Alu repetitive element
6028	18808	31798	0.83	2.0E-06	AI539448.1	EST_HUMAN	le5105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2000241 3' similar to TR:Q13537
6348	19118	32108	5.47	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7818	20513	33809	1.83	2.0E-06	AW869223.1	EST_HUMAN	w80504.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7988	20683	33809	0.57	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0087-120-400-002-402 SN0087 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H62051.1	EST_HUMAN	zh27c11.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9118	21804	34889	0.82	2.0E-06	AF003529.1	NT	y437c04.t1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:235074 5' similar to gb:X74629
9118	21804	34970	0.82	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9136	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
9600	22253	35438	1	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
9819	22470		0.83	2.0E-06	AV748989.1	EST_HUMAN	y16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12251	25357	30609	2.1	2.0E-06	P23249	SWISSPROT	yw68e03.s1 Soares_placenta_8to8weeks_2NkHP16c6W Homo sapiens cDNA clone IMAGE:257212 3'
32	12860	25477	2.36	1.0E-06	O76082	SWISSPROT	AV748989 NPC Homo sapiens cDNA clone NPCAXD05 5'
642	13421	26060	2.62	1.0E-06	AF084364.1	NT	PROTEIN MOV-1C
1434	14181	26866	1.61	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1514	14261	26947	1.67	1.0E-06	AL163278.2	NT	Mus musculus D6Mit56 protein (D6Mit56) mRNA, complete cds
1584	14311	26987	1.27	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1584	14311	26988	1.27	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21Q078
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	z00a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element
							z00a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element
							DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1987	14723	27443	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1987	14723	27444	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4336	17075	29703	12.81	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8804 Met protein (M8804 Met) gene, complete cds
5208	18016	30638	5.07	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-03:0700-002-006 BT0800 Homo sapiens cDNA
5232	18038	30666	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-06:0800-001-004 FN0004 Homo sapiens cDNA
5232	18038	30668	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-06:0800-001-004 FN0004 Homo sapiens cDNA
5389	18189	30881	1.22	1.0E-06	O60813	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5706	18500		0.78	1.0E-06	BE003527.1	EST_HUMAN	CM0-BT0281-03:1199-087-004 BT0281 Homo sapiens cDNA
6773	19517	32545	6.91	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7644	25427		0.63	1.0E-06	BE186330.1	EST_HUMAN	IL5-HT0730-02:0300-074-001 HT0730 Homo sapiens cDNA
7900	20595		0.77	1.0E-06	AA912623.1	EST_HUMAN	cd2x08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8171	20865	33987	1.2	1.0E-06	A1347010.1	EST_HUMAN	qp54e02.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8387	21080	34215	1.31	1.0E-06	A1287878.1	EST_HUMAN	q123f08.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9204	22083	35255	0.94	1.0E-06	N74635.1	EST_HUMAN	z155601.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296472 3'
9279	22033	35205	0.55	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9581	22234	35417	4.28	1.0E-06	U82688.1	NT	Homo sapiens shx gene, alternatively spliced products, complete cds
9581	22234	35418	4.28	1.0E-06	U82688.1	NT	Homo sapiens shx gene, alternatively spliced products, complete cds
9627	22280	35470	4.76	1.0E-06	AA132811.1	EST_HUMAN	z017608.r1 Strata gene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9688	22340		3.37	1.0E-06	AA449257.1	EST_HUMAN	z04411.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:785493 3' similar to
10365	23031		1.68	1.0E-06	AL163203.2	NT	gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11848	24245		3.85	1.0E-06	AW880941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
11724	24318	37641	1.38	1.0E-06	AA184914.1	EST_HUMAN	RC4-NT0054-120:500-012-503 NT0054 Homo sapiens cDNA
11724	24318	37642	1.38	1.0E-06	AA184914.1	EST_HUMAN	z04202.s1 Strata gene hnt neuron (#837233) Homo sapiens cDNA clone IMAGE:632364 3' similar to
12390	14723	27443	1.79	1.0E-06	AF184614.1	NT	SW:POL_SMSAV_P03359 POL POLYPROTEIN;
12390	14723	27444	1.79	1.0E-06	AF184614.1	NT	SW:POL_SMSAV_P03359 POL POLYPROTEIN;
351	13150	25790	2.24	9.0E-07	AF003528.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
351	13150	25791	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
8308	21000		0.93	9.0E-07	AL163280.2	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
11212	23875	37161	2.87	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C081

Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24326	37660	1.3	9.0E-07	AF087913.1	NT	Human endogenous virus retrovirus HIV-P-147D
4719	17451	30084	3.26	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soeris_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4719	17451	30085	3.26	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soeris_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5796	18587		9.43	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7901	20598		9.73	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		6.59	8.0E-07	T07770.1	EST_HUMAN	EST06660 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBEN89
11912	24476		8.22	8.0E-07	AL163260.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	18231	30944	0.72	7.0E-07	6005700	NT	Homo sapiens A TP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	6005700	NT	Homo sapiens A TP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	27352	2.98	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221069-024-011 CT0277 Homo sapiens cDNA
2498	15213	27656	4.52	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heparinase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3955	16705		1.83	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF-4P33 INTERGENIC REGION
9040	21730	34885	1.52	6.0E-07	BF001867.1	EST_HUMAN	7g84f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L;
11836	24420	37761	1.3	6.0E-07	BE063506.1	EST_HUMAN	CM0-BT0281-031199-067-003 BT0281 Homo sapiens cDNA
12158	25307		2.28	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1028-260300-121-112 NN1028 Homo sapiens cDNA
318	13121		1.94	5.0E-07	AI831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13795		4.25	5.0E-07	AA380630.1	EST_HUMAN	EST03615 Supt cells Homo sapiens cDNA 5' end
3028	15794		0.88	5.0E-07	AI831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2385547 3'
6029	18909	31769	0.9	5.0E-07	U65067.1	NT	Mus musculus O3-2 homeodomain protein (OG-2) gene, partial cds
6964	19446	32463	1.69	5.0E-07	AI393981.1	EST_HUMAN	lg08b06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107983 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
6964	19446	32464	1.69	5.0E-07	AI393981.1	EST_HUMAN	lg08b06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107983 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7248	19933	33008	17	5.0E-07	AW070885.1	EST_HUMAN	xs31ad1.x1 NCI_CGAP_B118 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U16341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33999	0.74	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8388	21081		0.82	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10265	22913	36123	4.94	5.0E-07	AI808587.1	EST_HUMAN	CM-BT178-220459-014 BT178 Homo sapiens cDNA



Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23256	36493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11500	24101	37413	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.62	5.0E-07	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12561	25211		3.48	5.0E-07	AW802837.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3981	16729	29364	2.02	4.0E-07	AW009802.1	EST_HUMAN	ws84h05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7078	19769		0.83	4.0E-07	AJ272286.1	NT	Homo sapiens SHP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7167	19854	32923	1.74	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7167	19854	32924	1.74	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7823	20518	33644	0.6	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8949	21640	34787	5.41	4.0E-07	AW418134.1	EST_HUMAN	xy46g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10027	22075	35890	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10027	22675	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10856	23338	36781	3.14	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2399703 3'
10856	23338	36782	3.14	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.68	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
431	13217	25882	9.64	3.0E-07	U19719.1	NT	Human microtubulin-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exon
598	13350	25978	2.12	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1353	14101	26776	2.67	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1622	14369		2.03	3.0E-07	M84857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2039	14773		1.42	3.0E-07	AA526763.1	EST_HUMAN	ns56b09.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains 1.13 L1 repetitive element;
2286	15011	27749	1.83	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2472	15190	27930	7.61	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-026300-001-f11 BN0115 Homo sapiens cDNA
2472	15190	27931	7.61	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-026300-001-f11 BN0115 Homo sapiens cDNA
3031	15787	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	yds012.f1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111895 6'
3157	15920	28586	1.45	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4711	17443	30075	0.86	3.0E-07	A1797236.1	EST_HUMAN	we86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5004	17727	30330	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14f09.s1 Strata gene lung (#637210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARAC-HIDONATE 12-LIPOXYGENASE (HUMAN)
5004	17727	30331	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14f09.s1 Strata gene lung (#637210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARAC-HIDONATE 12-LIPOXYGENASE (HUMAN)

Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5580	18377	31290	12.43	3.0E-07	O88907	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5883	18669	31610	0.83	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6603	18368		5.57	3.0E-07	AA815175.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7409	20086	33170	3.48	3.0E-07	AW787168.1	EST_HUMAN	cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338890 3'
7581	20231		0.79	3.0E-07	A1691065.1	EST_HUMAN	QV1-JM0036-20.0300-115-g02 UM0038 Homo sapiens cDNA
							tw28f1.1.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9028	21718	34873	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
11656	24253		1.75	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
12791	25043		5.1	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12855	25471	4.15	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
150	12965	26606	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
150	12965	26607	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	12969	26629	44.15	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	13505	26180	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	26181	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
922	13680	26353	3.73	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Strata gene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:950869 3' similar to gblL31890 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
923	13680	26354	2.15	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Strata gene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1140	13895	26556	1.37	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1596	14342	27032	2.96	2.0E-07	Q09701	SWISSPROT	HYPOTHEICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3676	16429	29070	15.93	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
6050	17778	30395	0.84	2.0E-07	AW070995.1	EST_HUMAN	xx05h07.x1 Source: NFI_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H12.1 CE00923 PROBABLE RABGAP DOMAINS ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5059	17778	30396	0.84	2.0E-07	AW070985.1	EST_HUMAN	xs05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
5280	18009	30694	1.21	2.0E-07	AW898066.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS
6456	25090	32223	0.81	2.0E-07	AW448988.1	EST_HUMAN	RC3-NN00068-210400-021-g11 NN0066 Homo sapiens cDNA
6565	19330	32337	1.79	2.0E-07	AI208715.1	EST_HUMAN	UIH-B13-ake-b-11-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2734008 3'
7588	20238	33342	0.67	2.0E-07	X95159.1	NT	qg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8369	21062		4.08	2.0E-07	AV729390.1	EST_HUMAN	H.sapiens brca2 gene exon 9
8595	21287	34426	0.97	2.0E-07	AA035198.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9661	22313		2.8	2.0E-07	AL163303.2	NT	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10167	22816	38033	5.41	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10396	23032	38245	0.9	2.0E-07	P00751	SWISSPROT	CM4-NN0003-260300-124-e08 NN0003 Homo sapiens cDNA
10398	23032	38248	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11871	24945		2.44	2.0E-07	BE163717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11953	25212		2.39	2.0E-07	AI732462.1	EST_HUMAN	PM0-HT0339-263100-008-H07 HT0339 Homo sapiens cDNA
1080	13838		1.97	1.0E-07	AL163282.2	NT	zn85h11.x5 Stratsgene lung carcinoma G37218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
2830	14259	28945	2.51	1.0E-07	P08266	SWISSPROT	RETROVIRUS-RELATED GAG POLYPEPTIDE (VERSION 1)
3727	13838		1.29	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4260	17001	29631	2.78	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4260	17001	29632	2.78	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4680	17424		0.93	1.0E-07	O78820	SWISSPROT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
5072	17791	30406	0.93	1.0E-07	AA019181.1	EST_HUMAN	ZINC FINGER PROTEIN 189
6410	19178	32177	0.87	1.0E-07	U82671.2	NT	zs56g02.t1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
6768	19512	32537	5.24	1.0E-07	BE047871.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	tz43406.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281339 5'
7392	20071	33150	9.08	1.0E-07	N56081.1	EST_HUMAN	tz43406.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2281339 5'
7548	20218	33320	0.67	1.0E-07	BF375909.1	EST_HUMAN	yv49c07.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:245484 3'
7548	20218	33321	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	PM4-TN0024-030800-002-b06 TN0024 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385	33499	0.64	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33941	2.73	1.0E-07	P67435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33942	2.73	1.0E-07	P67435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691	2.78	1.0E-07	AA693578.1	EST_HUMAN	z151e10.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9170	21840	35005	0.97	1.0E-07	P67110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9517	22170	35353	0.46	1.0E-07	BE327843.1	EST_HUMAN	h128h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9836	22487	35689	2.77	1.0E-07	BF874524.1	EST_HUMAN	MER18 repetitive element;
9844	22495	35696	1.21	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10362	23009		1.28	1.0E-07	AL163282.2	NT	EST185064 Brain IV Homo sapiens cDNA
12212	25188	30810	3.83	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12514	24864		1.87	1.0E-07	X51755.1	NT	h153c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O85722 O85722
7181	19867	32840	0.84	9.0E-08	AI539362.1	EST_HUMAN	DJ11163J1.1;
9787	22438	35645	1.88	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
11136	23804	37082	1.71	9.0E-08	AI891052.1	EST_HUMAN	h151b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11688	24263	37587	2.8	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABFB06 5'
12166	24646		4.44	9.0E-08	AJ251973.1	NT	wn30a07.x1 NCI_CGAP_Gee4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
593	15546		3.7	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element;
1028	13788		0.72	8.0E-08	BE795499.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3532	16288		1.53	8.0E-08	BE795499.1	EST_HUMAN	Homo sapiens partial steorh-1 gene
8638	21330	34474	3.05	8.0E-08	AI752387.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8638	21330	34475	3.05	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9527	22180	35364	2.93	8.0E-08	AW970693.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10461	23107	36338	0.47	8.0E-08	AF111167.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11211	23874		2.1	8.0E-08	AF293417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
78	12904	25542	2.66	7.0E-08	Q02357	SWISSPROT	EST382776 IMAGE: ressequences, MAGK Homo sapiens cDNA
1340	14088	26784	13.91	7.0E-08	X04909.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3563	16318	28985	1.15	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
							ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
							Rat mRNA for ribosomal protein L31
							DYNEIN HEAVY CHAIN (DYHC)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28966	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
11672	24267	37589	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus: Munc13-1 mRNA, complete cds
12019	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12019	16318	28966	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
798	13570	28230	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
798	13570	28231	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0168-19' 199-004-g09 HT0168 Homo sapiens cDNA
3059	15924	28469	0.81	6.0E-08	7692473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	29588	0.98	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7851	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21906		0.56	6.0E-08	AA827075.1	EST_HUMAN	cb56c05.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.B3 MER12 repetitive element ;
11391	23997	37299	2.24	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11520	24120		1.33	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
83	12609	25547	3.72	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2229	14957	27697	1.82	5.0E-08	AA493851.1	EST_HUMAN	nh03b08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
11914	24477		8.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12009	24509	31085	2.54	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1754	14496	27195	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1754	14496	27196	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2888	15655		1.09	4.0E-08	AL076581.1	EST_HUMAN	DKFZp43J0428_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43J0428 5'
3894	16644	28284	1.04	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6311	19082	32067	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8697	21389	34533	0.63	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9037	21727	34881	1.05	4.0E-08	L42571.1	NT	Citric acid cycle ribosomal transcription factor (UBF2) mRNA, complete cds
8545	22198		0.71	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		0.68	4.0E-08	AI016342.1	EST_HUMAN	at78d12.s1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622903 3'
10284	22932	36147	3.87	4.0E-08	AI050027.1	EST_HUMAN	en22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11009	23681	36639	1.71	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA,K-EXCHANGER.;
11009	23681	36640	1.71	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11031	23702	36669	4.02	4.0E-08	BF692493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER.;
11031	23702	36670	4.02	4.0E-08	BF692493.1	EST_HUMAN	G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11919	26334		4.31	4.0E-08	W76159.1	EST_HUMAN	z165g03.r1 Soares_fetal_heart_NH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.11 L1 repetitive element;
12549	24887		2.18	4.0E-08	AI349353.1	EST_HUMAN	1b95a11.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element;
5523	18321	31222	2.22	3.0E-08	BE018348.1	EST_HUMAN	b579a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17.;
6879	17955	30552	4.24	3.0E-08	AI792737.1	EST_HUMAN	q976f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944046 5'
7439	20116	33205	1.66	3.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
7849	20313		3.56	3.0E-08	AI498352.1	EST_HUMAN	1h93h09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9798	22449		0.52	3.0E-08	AF055066.1	NT	Homo sapiens MHC class 1 region
10948	23628	36877	1.32	3.0E-08	AI218001.1	EST_HUMAN	q121a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
11566	24165	37477	61.58	3.0E-08	R86279.1	EST_HUMAN	yp12b10.s1 Soares_breast_3NH8Bst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT- BINDING PROTEIN-1 (HUMAN);
11566	24165	37478	61.58	3.0E-08	R86279.1	EST_HUMAN	yp12b10.s1 Soares_breast_3NH8Bst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT- BINDING PROTEIN-1 (HUMAN);
11888	24459		2.27	3.0E-08	R18420.1	EST_HUMAN	yp02f04.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
201	13014		9.03	2.0E-08	AW302906.1	EST_HUMAN	xr67f06.x1 NCI_CGAP_Li26 Homo sapiens cDNA clone IMAGE:2767139 3'
221	13033		9.14	2.0E-08	AA425998.1	EST_HUMAN	zw48f07.r1 Soares_fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element/contains element MER15 repetitive element;
484	13269	25905	1.01	2.0E-08	AF198349.1	NT	Gallus gallus Dec2 protein (Dec2) mRNA, complete cds
845	13424	26062	13.62	2.0E-08	AW886438.1	EST_HUMAN	MFO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
845	13424	26063	13.62	2.0E-08	AW886438.1	EST_HUMAN	MFO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
989	13735		24.4	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138863 5'
1320	14069	26743	2.38	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1734	14476		12.18	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845198 5'

Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14585		4.11	2.0E-08	AW270271.1	EST_HUMAN	xp43f1.1x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2545	15260		1.71	2.0E-08	K00216.1	NT	Sheep His-tRNA-GUG
3202	15965	28618	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15965	28619	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	16561		1.76	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161098-012-b03 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ;
4903	17630		2.36	2.0E-08	AW572881.1	EST_HUMAN	het17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element ;
5549	18346	31255	1.19	2.0E-08	AA813204.1	EST_HUMAN	at80h11.s1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.93	2.0E-08	AW089824.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
7903	20508	33728	0.92	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8009	20704	33832	1.95	2.0E-08	AA490121.1	EST_HUMAN	ab02g08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8983	21073		0.9	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23062	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	yw7202.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10416	23062	36282	0.79	2.0E-08	N78097.1	EST_HUMAN	yw7202.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
12184	24958		1.54	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1499	15571	28631	1.16	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1768	14510	27211	1.45	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2044	14777		2.31	1.0E-08	BE141969.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	Homo sapiens hypoxan gene, exons 1-50
7668	20332	33443	1.28	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7834	20629	33756	0.52	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8026	20723	33855	0.64	1.0E-08	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8026	20723	33856	0.64	1.0E-08	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8445	21137	34276	1.94	1.0E-08	AJ015304.1	EST_HUMAN	at35a05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9104	21792		0.45	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9105	21783	34956	0.78	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-21C100-004-d02 BT0546 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9896	22516	35712	1.2	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN)(CTP)
10453	23099	36330	0.77	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11285	23946	37241	4.14	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12282	24715		2.82	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4218	16859	29583	4.85	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4218	16859	29584	4.85	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9862	22610		0.52	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
6390	19159		0.82	8.0E-09	AI270615.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7164	19851	32920	7.86	8.0E-09	AI183500.1	EST_HUMAN	qu86a11.x1 NCI_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978984 3' similar to contains L1.13 L1 repetitive element;
7899	20594	33726	2.85	8.0E-09	AW900159.1	EST_HUMAN	gd42a07.x1 Soares fetal heart NBH1H19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
8887	21578		2.85	8.0E-09	AA938892.1	EST_HUMAN	CMO-NN1004-100300-273-006 NN1004 Homo sapiens cDNA
3593	16346		1.73	7.0E-09	D86842.1	NT	op74d08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
7802	20497		0.91	7.0E-09	BF108755.1	EST_HUMAN	Homo sapiens DNA for 3-ketoad-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 contains MER29 b2 MER29 repetitive element;
7948	20841		0.82	7.0E-09	AA256200.1	EST_HUMAN	zr60c05.r1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
9159	21829	34993	2.91	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10083	22731	35946	1.42	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10244	22892		0.5	7.0E-09	AA058626.1	EST_HUMAN	z558e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381158 3' similar to contains L1.12 L1 repetitive element;
10571	23296		1.49	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2149	14879		0.99	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434C0514 5'
4922	17660	30263	3.12	6.0E-09	BE168421.1	EST_HUMAN	PM1-HT0527-160200-001-H05 HT0527 Homo sapiens cDNA
5296	18101	30760	11.59	6.0E-09	AW195784.1	EST_HUMAN	xn85f08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8475	21167	34311	0.93	6.0E-09	BE161663.1	EST_HUMAN	MF3-HT0446-260300-201-H12 HT0446 Homo sapiens cDNA
9074	21763	34925	1.96	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondrioplasia, thanatophoric dwarfism) (FGFR3) mRNA
10176	22824		3.76	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;



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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11798	24388	37722	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS003782 Human adult (K. Okubo) Homo sapiens cDNA
1394	14141	26818	3.27	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-110 HT0252 Homo sapiens cDNA
1845	14683	27298	1.06	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6316	19087	32071	1.73	5.0E-09	AA369454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
6748	17917	30581	0.76	5.0E-09	U6059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV9S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9V13S>
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
9995	22843	35855	2.22	5.0E-09	AW799867.1	EST_HUMAN	PM2-UM0053-240300-005-c08 UM0053 Homo sapiens cDNA
508	13292		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
944	13710		2.5	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1463	14200	26884	2.82	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2018	14751	27478	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2018	14751	27480	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2430	15151	27885	6.07	4.0E-09	AA350878.1	EST_HUMAN	EST168385 Inferred brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
7746	20442	33565	0.59	4.0E-09	AA495747.1	EST_HUMAN	z604c06.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8420	21113	34250	0.62	4.0E-09	T64642.1	EST_HUMAN	yf11a07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66804 3'
10779	23462	36704	2.06	4.0E-09	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
11011	23883	36943	1.47	4.0E-09	AI888401.1	EST_HUMAN	wm94f10.x1 NC_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11081	23731		1.93	4.0E-09	AA195142.1	EST_HUMAN	z34a12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807
2351	15073	27810	4.77	3.0E-09	BE222239.1	EST_HUMAN	DYNAMIN-1 (HUMAN); hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.k3
2557	15271	28006	1.2	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.k3
2656	15366	28104	1.13	3.0E-09	P23249	SWISSPROT	MER18 repetitive element; PROTEIN MOV-10
3323	16083	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.k3
3371	16130		1.08	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element; z654a04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:757422 5'
4076	16620		0.7	3.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4478	17211	29836	1.65	3.0E-09	Q973R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0983)

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7800	20485	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10147	22795	36009	1.7	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN. ;
10945	23624	36873	4.8	3.0E-09	BF108943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10945	23624	36874	4.8	3.0E-09	BF108943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
794	13566		2.43	2.0E-09	X16674.1	NT	7172c08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1235	13684	26653	7.99	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1655	14401		7.46	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2326	15051	27787	1.1	2.0E-09	O9Y3R5	SWISSPROT	DKFZp761B1710_1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761B1710 5'
3916	16688	26306	3.01	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KJAA0893)
5076	17795	30411	0.85	2.0E-09	M23161.1	NT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5633	18428	31341	0.55	2.0E-09	A1004062.1	EST_HUMAN	Human transposon-like element mRNA
6058	18638		0.67	2.0E-09	AL163249.2	NT	cd47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6682	18589		0.93	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7423	20100	33188	0.68	2.0E-09	W28834.1	EST_HUMAN	z63h06.r1 Soares_tad_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element
7717	20381	33494	0.62	2.0E-09	AW862126.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	MR1-CT0352-24(200-105-606 CT0352 Homo sapiens cDNA
11233	23696	37183	1.62	2.0E-09	AL163248.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12426	13566		22.07	2.0E-09	X16674.1	NT	Homo sapiens chromosome 21 segment HS21C048
12485	25403		2.41	2.0E-09	AA226070.1	EST_HUMAN	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12694	24934		1.75	2.0E-09	U82668.1	NT	nc11c02.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
1087	13845	26603	2.01	1.0E-09	5031624	NT	z179d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:L02882 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	13845	26504	2.01	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17	1.0E-09	AJ229041.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2892	15659	28304	1.59	1.0E-09	U80017.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
2926	15692	28336	3.25	1.0E-09	M28690.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
2926	15692	28337	3.25	1.0E-09	M28690.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3034	15800	28446	0.7	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds 601058602F1 NIF1_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'

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Table 4  
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476		6.4	1.0E-09	AA719297.1	EST_HUMAN	z135603.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5416	18215	30923	0.66	1.0E-09	AL163283.2	NT	Alu repetitive element; contains element MER22 repetitive element;
5740	18632	31455	1.89	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6053	18633	31795	3.13	1.0E-09	P26694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8289	20983	34124	0.85	1.0E-09	AI688474.1	EST_HUMAN	wc39505.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
10242	22660		2.92	1.0E-09	AL163283.2	NT	MER25.H1 MER25 repetitive element;
11799	24389		1.68	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12333	25344	30717	2.25	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12503	24957		1.35	1.0E-09	T83176.1	EST_HUMAN	ye24e05.r1 Stratiogene lung (#637210) Homo sapiens cDNA clone IMAGE:118888 5'
1286	14036	26707	3.74	9.0E-10	AW807740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2838	15906	28258	4.41	9.0E-10	AI870071.1	EST_HUMAN	wc79h03.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347258 3' similar to
							SW:RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element PTR5 repetitive element;
6735	19669	32901	4.76	9.0E-10	AI452982.1	EST_HUMAN	44509.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
142	12957	25599	13.27	8.0E-10	U63630.2	NT	TR:000372 000372 PUTATIVE P150.;
3337	18097	28748	0.88	8.0E-10	BE090748.1	EST_HUMAN	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
4177	16917	26544	3.17	8.0E-10	AA378832.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
9865	22515		2.44	8.0E-10	U36308.2	NT	EST89584 Small intestine I-Homo sapiens cDNA 5' and
685	13460	26107	9.36	7.0E-10	7706225	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
685	13460	26108	9.36	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1618	14365	27055	2.24	7.0E-10	Q13342	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
2013	14748		3.17	7.0E-10	P08548	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2564	15278		24.23	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3095	16950	28491	2.19	7.0E-10	X00856.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6092	18670	31836	4.18	7.0E-10	AA345220.1	EST_HUMAN	H.sapiens DHFR gene, exon 3
7316	19099	33078	1.08	7.0E-10	BF352883.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' and
7566	20226		1.48	7.0E-10	P35084	SWISSPROT	IL3-HT0619-110700-200-D12 HT0619 Homo sapiens cDNA
7875	20570	33696	1.6	7.0E-10	AF028701.2	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7875	20570	33697	1.6	7.0E-10	AF028701.2	NT	Homo sapiens preceritin-1 gene, exons 1 and 2
10209	22657	36073	1.67	7.0E-10	L08865.1	NT	Homo sapiens preceritin-1 gene, exons 1 and 2
							Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
893	13662	26327	3.5	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2684	15393	28132	1.21	6.0E-10	AI424405.1	EST_HUMAN	U22407.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4689	17423		2.7	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-03 1089-012-g12 CT0254 Homo sapiens cDNA
8682	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
8682	21374	34519	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9334	22187	35373	0.46	6.0E-10	P98073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
11950	24503		2.16	6.0E-10	AW971923.1	EST_HUMAN	EST384012 IMAGE resequences, MAGL Homo sapiens cDNA
745	13518		7.27	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5'
3468	16224	28878	2.5	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4931	17659	30269	1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7222	19907		1.51	5.0E-10	BF105199.1	EST_HUMAN	601822184F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4042413 5'
9436	22114	35288	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9436	22114	35289	1.89	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
109	12930		1.17	4.0E-10	AI221083.1	EST_HUMAN	cg08108.x1 Soares_placenta_8106weeks_2Nbr-IP8109W Homo sapiens cDNA clone IMAGE:175049 3'
567	13348	25076	0.74	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR.b2 LTR8 repetitive element;
1989	14725	27446	1.31	4.0E-10	AW594709.1	EST_HUMAN	rf64a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924648 3'
2580	15294	28032	3.73	4.0E-10	AL163303.2	EST_HUMAN	hg58g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
7076	19767	32831	26.71	4.0E-10	AF224099.1	NT	Homo sapiens of rrmosome 21 segment HS21C103
10095	22743	35957	0.49	4.0E-10	AW293243.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10343	22960	36208	0.89	4.0E-10	AI287342.1	EST_HUMAN	U1-H-B12-ah1-a-07-Q.U.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3'
895	13663	26329	3.55	3.0E-10	N36113.1	EST_HUMAN	sq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035683
1329	14078		4.72	3.0E-10	AY005160.1	NT	y93206.s1 Soares_melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:272983 3' similar to contains L1.1 L1 repetitive element;
4498	17234	29864	1.04	3.0E-10	AL163203.2	NT	Homo sapiens extracellular glycoprotein keratin precursor, gene, complete cds
4498	17234	29865	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5365	18169	30855	1.24	3.0E-10	N60109.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6110	18887	31856	2.52	3.0E-10	P20350	SWISSPROT	yz11g08.s1 Soares_multiple_sclerosis_2Nbr-HMSP Homo sapiens cDNA clone IMAGE:282782 3'
6258	19032	32007	3.43	3.0E-10	BE302970.1	EST_HUMAN	RHOMBLOID PROTEIN (VEINLET PROTEIN)
							ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'

Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7680	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7680	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8629	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	ye74b12.a1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8947	21638	34784	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-16C200-064-B06 CT0219 Homo sapiens cDNA
8947	21638	34785	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-16C200-064-B06 CT0219 Homo sapiens cDNA
9240	21919		0.58	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10359	23006		2.37	3.0E-10	T65891.1	EST_HUMAN	ye11e12.r1 Straiogene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
10493	23139		1.34	3.0E-10	AA769294.1	EST_HUMAN	nz35g03.a1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289808 3'
12584	24907	31003	2.05	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
34	12862	25479	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12862	25480	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14827		1.06	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nab) and survival motor neuron protein (smn) genes, complete cds
2985	15751		1.04	2.0E-10	BF676047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5714	18507		2.64	2.0E-10	Q28940	SWISSPROT	(HPRG)
6156	18933	31900	1.37	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	19963	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	807586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7912	20607	33737	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7912	20607	33738	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434595.1	EST_HUMAN	7a78d08.x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11297	23958		1.37	2.0E-10	AJ862153.1	EST_HUMAN	ba10f12.x1 Soares fetal Nb2HF8 sw Homo sapiens cDNA clone IMAGE:2043665 3'
1498	14245		1.87	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-280300-001-401 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AV682123.1	EST_HUMAN	AV682123 GLC Homo sapiens cDNA clone GLOCXA11 3'
2586	15300		3.16	1.0E-10	AW862001.1	EST_HUMAN	QV0-CT0225-191199-058-408 CT0225 Homo sapiens cDNA
3481	16247	28801	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.7	1.0E-10	AL041085.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041085.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3896	16744		6.19	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4108	18851	28477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4108	18851	28478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4113	18858	28484	1.84	1.0E-10	AB031089.1	NT	Homo sapiens P10X1 mRNA for protein containing GXXG domain 1, complete cds
4149	18891		1.84	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	A1797745.1	EST_HUMAN	web2104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.1 MER31 repetitive element;
6720	19035	32678	0.66	1.0E-10	AF003428.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375	20055		0.65	1.0E-10	P08648	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7683	20251	33357	0.55	1.0E-10	AU128594.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138	20632	33968	1.04	1.0E-10	AW408980.1	EST_HUMAN	fb_BA4 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	A1268340.1	EST_HUMAN	qm04e10.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1890874 3' similar to contains L1.11 L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.l1 Stratigene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36754	2.85	1.0E-10	A038280.1	EST_HUMAN	oy65f03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672861 3'
11896	17913		1.71	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	BE145800.1	EST_HUMAN	IL2-HT0203-291099-018-c08 HT0203 Homo sapiens cDNA
2097	14828	27561	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	14828	27562	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28795	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
4465	17201	29827	1.03	9.0E-11	AA775985.1	EST_HUMAN	ae7801.s1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:970237 3'
5487	18286		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10054	22702	35919	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-508508 5'
3114	15879		8.33	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3945	16805	29334	0.7	8.0E-11	A479617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4022	16768	29398	4.88	8.0E-11	N23712.1	EST_HUMAN	yw49e06.s1 Wellman Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255238 3'
6674	19338		0.65	8.0E-11	AW166158.1	EST_HUMAN	xl45h11.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1430	14177	26862	1.75	7.0E-11	AA330642.1	EST_HUMAN	MER10 repetitive element;
							EST34392 Embryo, 6 week   Homo sapiens cDNA 5' end
3852	16802	28240	1.03	7.0E-11	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8396	21089	34224	2.05	7.0E-11	AF163894.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22777		1.17	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
403	13188	25837	7.01	6.0E-11	M55270.1	NT	Human matrix Glu protein (MGP) gene, complete cds
403	13188	25838	7.01	6.0E-11	M55270.1	NT	Human matrix Glu protein (MGP) gene, complete cds
6622	16384	32398	0.67	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7593	20261	33369	3.65	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8262	20958	34085	7.81	6.0E-11	AV1727859.1	EST_HUMAN	AV1727859 HTC Homo sapiens cDNA clone HTCCASC06 5'
9213	21892	35059	0.52	6.0E-11	BE063608.1	EST_HUMAN	CMO-BT0281-031169-067-403 BT0281 Homo sapiens cDNA
11	12638	25451	1.49	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3359	12638	25451	1.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4203	16944	26671	1.36	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6423	19191	32187	1.63	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7430	20107	33194	14.05	5.0E-11	11415799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1380	14127		1.94	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2793	15498	26238	7.14	4.0E-11	BE985900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
2969	15735	26385	1.16	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4576	17311	29939	0.85	4.0E-11	D44688.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6394	19153	32153	3.2	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6903	19641	32686	0.82	4.0E-11	AA442830.1	EST_HUMAN	zv58f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR-G1055250
7274	19958		4.5	4.0E-11	AF224609.1	NT	G1055250 PHEROMONE RECEPTOR VN4. ; Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9295	21962		1.79	4.0E-11	BE149425.1	EST_HUMAN	UC1-HT0258-21C100-013-408 HT0258 Homo sapiens cDNA
8592	22215	35402	0.9	4.0E-11	AI609753.1	EST_HUMAN	tt82g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP-ZK353.1 CE00385 ;

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12462	24830	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1475	14222	26908	2.8	3.0E-11	0679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nm2), mRNA
4243	16984		1.04	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	A1150502.1	EST_HUMAN	q38c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1162	13916	26580	3.99	2.0E-11	R24807.1	EST_HUMAN	Y943e12.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1162	13918	26581	3.99	2.0E-11	R24807.1	EST_HUMAN	Y943e12.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1808	14354	27042	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1808	14354	27043	4.86	2.0E-11	L17432.1	NT	COR3 beta (COR3beta) genes, complete cds
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3 beta (COR3beta) genes, complete cds
1812	14359	27048	1.21	2.0E-11	A126371.1	EST_HUMAN	qc51c10.x1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
3191	15954	28607	7.58	2.0E-11	P10263	SWISSPROT	gb:U02832 PEROKISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.t1
3320	16080	28730	1.11	2.0E-11	A478617.1	EST_HUMAN	L1 repetitive element;
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							tm64c09.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
							POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-
3356	16116	28771	0.93	2.0E-11	Q10473	SWISSPROT	ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
3488	16244		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4409	17146		0.68	2.0E-11	BE065837.1	EST_HUMAN	RC3-BT0316-170-200-014-e05 BT0316 Homo sapiens cDNA
4567	17302		0.72	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4882	17609		1.77	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-2611099-014-e01 BT0258 Homo sapiens cDNA
6044	18824	31785	1.02	2.0E-11	AW877806.1	EST_HUMAN	QV2-PT0073-280300-109-108 PT0073 Homo sapiens cDNA
6216	18992	31968	1.87	2.0E-11	AA681028.1	EST_HUMAN	nc83h05.t1 NC1_CGAP_GCI Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7065	19784	32850	0.59	2.0E-11	BF592945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.;
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	797603.x1 NC1_CGAP_GCI Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9123	21811		1.14	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10184	22832	36048	5.44	2.0E-11	Q13608	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10413	23059	36277	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-e11 OT0072 Homo sapiens cDNA
10413	23059	36278	1.12	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-e11 OT0072 Homo sapiens cDNA



Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726	36307	1.48	2.0E-11	AA035369.1	EST_HUMAN	zK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11056	23728	36898	1.48	2.0E-11	AA035368.1	EST_HUMAN	zK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11080	23760	37035	1.57	2.0E-11	AA281956.1	EST_HUMAN	zs18b04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685619 5'
12017	26332		1.54	2.0E-11	AA704195.1	EST_HUMAN	zJ77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048	24567		3.54	2.0E-11	AW842143.1	EST_HUMAN	RC00-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-073900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D28217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417986	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	26078	1.34	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1195	13947	26811	3.35	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1495	14232		2.36	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14765	27494	1.13	1.0E-11	P16268	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
3490	16246	28900	1.2	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5249	18055	30683	16.93	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18533	31456	0.63	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
8101	20795	33926	3.15	1.0E-11	4885546	NT	MER10 repetitive element;
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8946	21637	34782	1.89	1.0E-11	BF365119.1	EST_HUMAN	y73408.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28166 5'
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11267	23919	37212	1.62	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
9097	22348	35542	1.07	9.0E-12	AL163300.2	NT	602164807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
9097	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9237	21916		0.93	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12125	24617		3.91	8.0E-12	AJ271736.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4613	17348	28982	1.16	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11322	24013	37316	9.59	7.0E-12	AA704735.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3535	16291		0.71	6.0E-12	AV730554.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
4314	17063	29678	8.52	6.0E-12	AA732616.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAFW06 5'
6296	19086	32051	0.77	6.0E-12	AF020503.1	NT	nz28811.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21585	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9374	21949		1.67	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1020	13780	26442	3.52	5.0E-12	T08573.1	EST_HUMAN	MER29 repetitive element:
3385	16144	26801	1.61	5.0E-12	BE047778.1	EST_HUMAN	EST04462 Fetal brain, Stragene (catt936209) Homo sapiens cDNA clone HFBDV33
3713	18466	29104	5.03	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCL_CGAP_Bm82 Homo sapiens cDNA clone IMAGE:2291217 5'
5931	18715	31671	6.41	5.0E-12	AL163278.2	NT	Homo sapiens Xq1 pseudautosomal region; segment 2/2
5931	18715	31672	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	19168	32167	11.33	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6933	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST138850 MAG3E resequences, MAGN Homo sapiens cDNA
6942	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1815_s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1815 3'
8128	20822	33959	1.33	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1815_s1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B1815 3'
8588	21258		0.65	5.0E-12	AW897037.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart_NbH110W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1.1 repetitive element:
8893	21584		0.54	5.0E-12	AL079681.1	EST_HUMAN	RC1-OT00886-220300-011-507 OT0089 Homo sapiens cDNA
9006	21896	34947	2.83	5.0E-12	ALJ271735.1	NT	DKFZp434J0428_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0428 5'
9323	21990	35161	0.96	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq1 pseudautosomal region; segment 1/2
10175	22823		4.45	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10262	22910	36120	0.76	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
10468	23114	36344	0.44	5.0E-12	6978764	NT	Homo sapiens chromosome 21 segment HS21C102
237	13047	25688	4.2	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homodog) (Doc), mRNA
238	13047	25688	4.03	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4577	17312	29940	0.8	4.0E-12	AI689984.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
7619	20190		0.72	4.0E-12	BF445140.1	EST_HUMAN	b22b05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE:
8141	20835		3.2	4.0E-12	AF109007.1	NT	ned21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2
8587	21279	34418	0.87	4.0E-12	AB042815.1	NT	MER7 repetitive element:
11019	23091	36954	4.2	4.0E-12	AJ229043.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12375	24774		2.76	4.0E-12	U78027.1	NT	Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	26011	4.27	3.0E-12	AW341683.1	EST_HUMAN	h13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR-O14517 O14517 SMRP.;
602	13380	26012	4.27	3.0E-12	AW341683.1	EST_HUMAN	h13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR-O14517 O14517 SMRP.;
5084	17803	30421	0.81	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
5365	18167	30853	1.52	3.0E-12	AF111168.2	NT	Homo sapiens uridine phosphorylase, subunit II gene, complete cds; and unknown genes
7654	20318		0.63	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0255-031099-011-h02 CT0255 Homo sapiens cDNA
8273	20967	34109	0.51	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
9004	21694	34844	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10551	23247	38483	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10551	23247	38484	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1649	14395	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120-005-005 UM0071 Homo sapiens cDNA
4094	16838	29462	0.91	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4094	16838	29463	0.91	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4367	17124		2.03	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031169-087-003 BT0281 Homo sapiens cDNA
4840	17570	30192	1.18	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4840	17570	30193	1.18	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
							RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
5168	17978	30491	0.77	2.0E-12	P11369	SWISSPROT	EST383946 MAGL Homo sapiens cDNA
6386	19154		2.8	2.0E-12	AW971857.1	EST_HUMAN	EST06080 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end
7075	19786	32830	3.74	2.0E-12	T08169.1	EST_HUMAN	MR0-HT0559-201400-015-008 HT0559 Homo sapiens cDNA
7244	19929	33005	1.02	2.0E-12	BE173035.1	EST_HUMAN	Homo sapiens Ac-like transposable element (ALTE), mRNA
7558	20228	33331	2.2	2.0E-12	11422228	NT	Homo sapiens purative BPES syndrome breakpoint region protein gene, complete cds
9208	22087		1.84	2.0E-12	AF186864.1	NT	MR3-HT0487-15(200-113-g01 HT0487 Homo sapiens cDNA
9885	22535		11.12	2.0E-12	BE166860.1	EST_HUMAN	qq07702.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1631835 3' similar to TR-Q13538
10412	23058	36276	0.87	2.0E-12	A1334130.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN. ;
12032	24557		2.81	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12223	24680		2.5	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
119	12838	25579	2.21	1.0E-12	AW627674.1	EST_HUMAN	h190409.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.1
1980	14716		1.39	1.0E-12	A1871726.1	EST_HUMAN	MER18 repetitive element ;
3067	15833	28476	1.29	1.0E-12	AF000991.1	NT	wn51107.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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Table 4  
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3067	15633	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	16605	29242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RF3 Homo sapiens cDNA clone NT2RF3004070 5'
3855	16605	29243	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RF3 Homo sapiens cDNA clone NT2RF3004070 5'
5877	16603		2.25	1.0E-12	U62828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5860	18732		1.93	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0061
6438	19206	32202	0.62	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7018	19708	32764	2.07	1.0E-12	AF108864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7050	19741	32802	11.32	1.0E-12	A1248533.1	EST_HUMAN	qf06a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1840614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
7050	19741	82803	11.32	1.0E-12	A1248533.1	EST_HUMAN	qf06a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1840614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
8606	21298	34442	1.16	1.0E-12	AA782323.1	EST_HUMAN	ac26a05.x1 Stratagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11273	23634		1.72	1.0E-12	AW468478.1	EST_HUMAN	he38f07.x1 NCL CGAP_GML1 Homo sapiens cDNA clone IMAGE:2921317 3' similar to contains element LTR3 repetitive element;
11942	24497	37809	4.64	1.0E-12	AW982164.1	EST_HUMAN	EST374237 MAGG: resequenced, MAGG Homo sapiens cDNA
12150	24637		1.62	1.0E-12	A1738592.1	EST_HUMAN	w631h08.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12294	25308		2.92	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
3618	16371		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq1 pseudautosomal region, segment 1/2
3927	16677	29320	0.96	9.0E-13	AB029900.1	NT	Homo sapiens CS1 gene for carbonyl sulfide transferase, exon 1, 2, 3, 4, 5
9501	22154		2.07	9.0E-13	N69653.1	EST_HUMAN	za26b06.x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:263651 3'
700	13475	26123	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	13475	26124	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1830	14569	27281	2.94	8.0E-13	U60017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8011	20708	33834	0.78	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8011	20708	33835	0.76	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10046	22664		3.08	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Table 4

## Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.87	8.0E-13	U66080.1	NT	Human germ-line T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S8A3N2T, TCRBV13S6A2T, TCRBV6S8A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
7718	20382	33495	0.71	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCJ CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2437601.3
7718	20382	33498	0.71	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCJ CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2437601.3
8133	20827		0.56	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3669813.5
12617	24823		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAc-T1)
2094	14825	27558	6.75	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3316	18076		0.74	5.0E-13	R78338.1	EST_HUMAN	y82b04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145760.5
3392	19151		1.54	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350.3 similar to contains Alu repetitive element; contains element MER22 repetitive element;
6777	19521	32548	0.84	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10767	23451	36893	2.72	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1880	14598		2.23	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221399-001-e11 HT0224 Homo sapiens cDNA
2482	15180		1.67	4.0E-13	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
5498	18297	31195	5.51	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7105	19783	32858	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7512	20183	33277	0.94	4.0E-13	AA431828.1	EST_HUMAN	zw76g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182.5 similar to TR:G452763
7620	20286		1.07	4.0E-13	N44291.1	EST_HUMAN	y33g05.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273080.5 similar to PIR:A32895
8740	21432	34577	1.07	4.0E-13	AL043810.1	EST_HUMAN	A32895 t complex sterility protein - mouse;
9402	22084	35235	0.45	4.0E-13	AA078907.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: hhas3) Homo sapiens cDNA clone DKFZp434A0128.6
9819	22568	35764	4.94	4.0E-13	A1289831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11120	23789	37066	2.09	4.0E-13	AA435819.1	EST_HUMAN	q132d05.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945.3 similar to contains Alu repetitive element;
11120	23789	37067	2.09	4.0E-13	AA435819.1	EST_HUMAN	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514.3
175	12987		4.94	3.0E-13	AF003528.1	NT	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514.3
845	13815		1.62	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							zw68g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406.5

Table 4

## Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15062	27831	1.26	3.0E-13	AL271736.1	NT	Homo sapiens Xq pseudotribosomal region; segment 2/2
2483	15201		2.47	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2669	15378	28117	2.91	3.0E-13	BF372982.1	EST_HUMAN	OM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3182	15945		2.97	3.0E-13	AA745844.1	EST_HUMAN	db18d02.s1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1324035 3'
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element;
5902	18687	31635	0.62	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
7783	20478	33603	7.67	3.0E-13	U52111.2	NT	O75139 KIAA0844 PROTEIN. ; Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20670	33782	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
7975	20970	33793	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
10098	22746	35961	0.72	3.0E-13	AW835487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10675	23270		3.61	3.0E-13	AJ084788.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	36004	3.96	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-03-1199-087-003 BT0281 Homo sapiens cDNA
11598	24197	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
145	12960	25602	3.42	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
232	13043	25683	2.06	2.0E-13	U23839.1	NT	Denio rat fibroblast growth factor receptor 4 mRNA, complete cds
1247	13906	26663	7.99	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	26419	0.9	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	26420	0.9	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	16036	26686	1.13	2.0E-13	BF431890.1	EST_HUMAN	na076705.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3498	16254	26908	1.11	2.0E-13	AF109607.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4098	18631		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	18812	31772	4.7	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.58	2.0E-13	X79417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6717	19632	32675	7.15	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type B-phosphofructokinase (EC 2.7.1.11) exon 2
6864	19436	32461	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
6954	19436	32452	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	36219	3.87	2.0E-13	5031896	NT	Homo sapiens mal-21 (C. elegans)-like 1 (MAB21L1) mRNA
12106	24602		3.48	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
285	13091	25732	1.52	1.0E-13	S74128.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
868	13637	26307	5.84	1.0E-13	AJ007973.1	NT	Homo sapiens LGI4/D2B gene
1313	14061	26736	1.08	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4553	17288	29917	1.84	1.0E-13	BF340887.1	EST_HUMAN	THR repetitive element ; 602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5'
7810	20505	33626	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
7810	20505	33627	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
9990	22638		0.79	1.0E-13	O15481	EST_HUMAN	repetitive element; contains element MER24 repetitive element ;
10189	22847	36063	0.53	1.0E-13	AF300701.1	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11934	24492		2.25	1.0E-13	AV716377.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.t2 MER29 repetitive element ;
12563	24893		2.12	1.0E-13	AJ271735.1	NT	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
324	13125	25761	1.81	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2 aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
325	13126	25762	3.05	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2504	15221		3.68	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-060100-013-d09 CT0322 Homo sapiens cDNA
2599	15313	28050	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2599	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15463	28206	2.6	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3109	15874	28513	3.96	9.0E-14	AW513286.1	EST_HUMAN	xo54h05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707833 3'